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Om nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:28:49 ; Search time 459.432 Seconds
3338.794 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267 Sequence: 1 tacatggagtaaagacccct.....agtagttggggatcgcccc 267

Scoring table: ORIGO_NUC Gapop_60.0 , Gapext 60.0

Searched: 3625171 seqs, 2700493622 residues

Word-size: 10-

Total number of hits satisfying chosen parameters: 796812

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Published_Applications_NA:*

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21: /cgn2_6/ptodata/2/pubnra/us60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 5	35	13.1	54	16	US-10-329-624-5036
c 6	35	13.1	187	8	US-08-781-986A-4682
c 7	35	13.1	187	16	US-10-329-624-4682
c 8	35	13.1	216	8	US-08-781-986A-4589
c 9	35	13.1	216	16	US-08-781-986A-4589
c 10	35	13.1	221	8	US-08-781-986A-4572
c 11	35	13.1	221	16	US-10-329-624-4572
c 12	35	13.1	235	8	US-08-781-986A-4536

c 13	35	13.1	235	16	US-10-329-624-4536	Sequence 4536, AP
c 14	35	13.1	242	8	US-08-781-986A-4538	Sequence 4538, AP
c 15	35	13.1	242	16	US-10-329-624-4538	Sequence 4538, AP
c 16	35	13.1	283	8	US-08-781-986A-4460	Sequence 4460, AP
c 17	35	13.1	283	16	US-10-329-624-4460	Sequence 4460, AP
c 18	35	13.1	295	8	US-08-781-986A-4440	Sequence 4440, AP
c 19	35	13.1	300	8	US-08-781-986A-4416	Sequence 4416, AP
c 20	35	13.1	300	16	US-10-329-624-4416	Sequence 4416, AP
c 21	35	13.1	309	8	US-08-781-986A-4326	Sequence 4326, AP
c 22	35	13.1	309	16	US-10-329-624-4326	Sequence 4326, AP
c 23	35	13.1	327	8	US-08-781-986A-4342	Sequence 4342, AP
c 24	35	13.1	327	16	US-10-329-624-4342	Sequence 4342, AP
c 25	35	13.1	330	8	US-08-781-986A-4324	Sequence 4324, AP
c 26	35	13.1	330	16	US-10-329-624-4324	Sequence 4324, AP
c 27	35	13.1	338	8	US-08-781-986A-4246	Sequence 4246, AP
c 28	35	13.1	338	16	US-10-329-624-4246	Sequence 4246, AP
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c 30	35	13.1	340	16	US-10-329-624-4196	Sequence 4195, AP
c 31	35	13.1	348	8	US-08-781-986A-4176	Sequence 4176, AP
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c 42	35	13.1	371	16	US-10-329-624-4118	Sequence 4118, AP
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c 44	35	13.1	371	16	US-10-329-624-4118	Sequence 4118, AP
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c 47	35	13.1	386	16	US-10-329-624-4064	Sequence 4064, AP
c 48	35	13.1	389	8	US-08-781-986A-3890	Sequence 3890, AP
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c 73	35	13.1	400	16	US-10-329-624-3645	Sequence 3645, AP
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c 75	35	13.1	400	16	US-10-329-624-3660	Sequence 3660, AP
c 76	35	13.1	400	16	US-10-329-624-3661	Sequence 3661, AP
c 77	35	13.1	400	16	US-10-329-624-3661	Sequence 3661, AP
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c 80	35	13.1	400	16	US-10-329-624-3711	Sequence 3711, AP
c 81	35	13.1	400	16	US-10-329-624-3718	Sequence 3718, AP
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c 83	35	13.1	400	16	US-10-329-624-3744	Sequence 3744, AP
c 84	35	13.1	400	16	US-10-329-624-3744	Sequence 3744, AP
c 85	35	13.1	400	16	US-10-329-624-3768	Sequence 3768, AP

RESULT 1
US-09-070-927A-359/c
Sequence 359, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8304
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 550:
SEQUENCE CHARACTERISTICS:
LENGTH: 9797 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 550:
US-09-070-927A-550

RESULT 2
US-09-070-927A-550/c
Sequence 550, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
CITY: Rockville
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,927A
FILING DATE: 04-May-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/046,655
FILING DATE: 1997-05-16
APPLICATION NUMBER: 60/066,009
FILING DATE: 1997-11-14

ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PB369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8304
TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 550:
SEQUENCE CHARACTERISTICS:
LENGTH: 9797 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 550:
US-09-070-927A-550

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Best Local Similarity 100.0%; Pred. No. 4.7e-14;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 GAAGGATACATGCCATGCCAACAGAGTTAGCTTC 236
Db 9424 GAAGGATACACTGTCCCATGCCAACAGAGTTAGCTTC 9381

RESULT 3
US-09-070-927A-345
Sequence 345, Application US/09070927A
Patent No. US20020120116A1
GENERAL INFORMATION:
APPLICANT: Charles A. Kunsch
Patrick J. Dillon
Steven Barash

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
NUMBER OF SEQUENCES: 982

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OM nucleic - nucleic search, using SW model

Run on: November 15, 2004, 14:18:54 ; Search time 113.856 seconds

(without alignments) 166.850 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tatatggagtaaagccct..... agtagttggggatcgcccc 267

Scoring table: Oligo.NUC_

Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 35539441 residues

Word size: 10

Total number of hits satisfying chosen parameters: 100240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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13	35	13.1	242	4 US-08-781-986A-4538 Sequence 4538, AP
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21	35	13.1	309	4 US-08-781-986A-4326 Sequence 4326, AP
22	35	13.1	327	4 US-08-956-171B-4342 Sequence 4342, AP
23	35	13.1	327	4 US-08-781-986A-4342 Sequence 4342, AP
24	35	13.1	330	4 US-08-956-171B-4324 Sequence 4324, AP
25	35	13.1	330	4 US-08-781-986A-4324 Sequence 4324, AP
26	35	13.1	338	4 US-08-781-986A-4246 Sequence 4246, AP
27	35	13.1	338	4 US-08-781-986A-4246 Sequence 4246, AP

Result No.	Score	Query Match Length	DB ID	Description
1	44	16.5	249	4 US-09-154-000-314B sequence 314B, AP
2	35	13.1	54	4 US-08-956-171B-5036 Sequence 5036, AP
3	33	13.1	54	4 US-08-781-986A-5036 Sequence 5036, AP
4	35	13.1	187	4 US-08-956-171B-4682 Sequence 4682, AP
5	35	13.1	187	4 US-08-781-986A-4682 Sequence 4682, AP
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7	35	13.1	216	4 US-08-781-986A-4589 Sequence 4589, AP
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9	35	13.1	221	4 US-08-781-986A-4572 Sequence 4572, AP
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11	35	13.1	235	4 US-08-781-986A-4536 Sequence 4536, AP
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13	35	13.1	242	4 US-08-781-986A-4538 Sequence 4538, AP
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17	35	13.1	295	4 US-08-781-986A-4440 Sequence 4440, AP
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19	35	13.1	300	4 US-08-781-986A-4415 Sequence 4415, AP
20	35	13.1	309	4 US-08-956-171B-4326 Sequence 4326, AP
21	35	13.1	309	4 US-08-781-986A-4326 Sequence 4326, AP
22	35	13.1	327	4 US-08-956-171B-4342 Sequence 4342, AP
23	35	13.1	327	4 US-08-781-986A-4342 Sequence 4342, AP
24	35	13.1	330	4 US-08-956-171B-4324 Sequence 4324, AP
25	35	13.1	330	4 US-08-781-986A-4324 Sequence 4324, AP
26	35	13.1	338	4 US-08-781-986A-4246 Sequence 4246, AP
27	35	13.1	338	4 US-08-781-986A-4246 Sequence 4246, AP

TELECOMMUNICATION INFORMATION
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

KOSULI: T
US-09-134-000C-3148
; Sequence 3148, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al

FILE REFERENCE: 032196-032
 TITLE OF INVENTION: ENTEROCOCCUS FABCAIS FOR DIAGNOSTICS AND THERAPEUTICS
 CURRENT APPLICATION NUMBER: US/09/134,00C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-03-15
 NUMBER OF SEQ ID NOS: 6A12

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Qy	Matches	100.0%	0	0
Qy	Matches	35	0	0
Db	Conservative	0	0	0
Db	Mismatches	0	0	0
Db	Indels	0	0	0
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52	ACACCTGTTCCATGCGAACAGAGTAACT	18		

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 Best Local Similarity 100.0%; pred. No. 1.5e-09;
 Matches 35; Conservative 0; Mismatches 0;
 Qy 200 ACACCTGTTCCATGGAAACAGAGT-TAAGCT 234
 Ds ||||||| ||||| ||||| ||||| ||||| Indels 0;
 52 ACACCTGTTCCATGGAAACAGAGT-TAAGCT 18 gaps 0;

; Software: PatentUS VERSION 3.1
; SEQ ID NO: 3148
; LENGTH: 249
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-3148

Query Match : 16.5%; Score 44; DB 4; Length 249;

RESULT 3.
US-08-781-986A-5036/C
; Sequence 5036, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch

	Matches	44;	Conservative	0;	Mismatches	0;	Indels
Oy	193	GAAGGATACCTGTGCCATGCGGACACAGAGCTTAAGCTC			236		
Db	48	GAAGGATACCTGTCCATGCCGACACKGAAGCTTAAGCTC			91		

RESULT 2
TTS-08-956-171E-5036/c

; patent No. 6593114
; GENERAL INFORMATION:

Patrick S. Dil
Craig A. Rosen

TITLE OF INVENTION: Michael R. Hamton
Staphylococcus aureus Polynucleotides and Sequences

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue

COUNTRY: USA
ZIP: 20850

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB24881

Pre^d. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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GenCore - version 5.1.6

nucleic - nucleic search, using sw model

on: November 15, 2004, 11:59:59 ; Search time 517.162 Seconds

US-10-088-666-1

Effect score: 267

Sequence: tataatggaaagttaagacccat.....agtagttggggatcgcccc 267

String table: Ötlico_NUC_

Gapop_60_0 , Gapext 60.0

Length: 0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing First 100 summaries

No.	Score	Query Match Length	DB ID	Description
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2	73	27.3	AABF61567	Aaf61567 Lactobaci
3	50	18.7	AABF61570	Aaf61570 Lactobaci
4	50	18.7	AABF61568	Aaf61568 Lactobaci
5	50	18.7	AABF61569	Aaf61569 Lactobaci
6	44	16.5	AABH8263	Adbb5263 Enterococ
7	44	16.5	AAXL13296	Aaxl1296 Enterococ
8	44	16.5	AAS99091	Abs99091 Enterococ
9	44	16.5	AAXL13487	Aaxl1487 Enterococ
10	44	16.5	AAS9982	Abs9982 Enterococ
11	44	16.5	AAXL13282	Aaxl1282 Enterococ
12	44	16.5	AAS99077	Abs99077 Enterococ
13	44	16.5	ADEF77343_05	Continuation (6 of 16)
14	44	16.5	ADEF77343_07	Continuation (8 of 16)
15	44	16.5	ADEF77343_18	Continuation (19 of 24)
16	40	15.0	AABF61572	Aaf61572 L. casei
17	40	15.0	AABF61571	Aaf61571 L. casei
18	40	15.0	AABF61575	Aaf61575 Pediococc
19	40	15.0	AABF61574	Aaf61574 Pediococc
20	40	15.0	ABL154766	Ab154766 Pediococc
21	35	13.1	AAV79347	Aav79347 Staphyloc

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Summary	Score	Length	DB ID	Description
1	267	100.0	AABF61566	Aaf61566 Lactobaci
2	73	27.3	AABF61567	Aaf61567 Lactobaci
3	50	18.7	AABF61570	Aaf61570 Lactobaci
4	50	18.7	AABF61568	Aaf61568 Lactobaci
5	50	18.7	AABF61569	Aaf61569 Lactobaci
6	44	16.5	AABH8263	Adbb5263 Enterococ
7	44	16.5	AAXL13296	Aaxl1296 Enterococ
8	44	16.5	AAS99091	Abs99091 Enterococ
9	44	16.5	AAXL13487	Aaxl1487 Enterococ
10	44	16.5	AAS9982	Abs9982 Enterococ
11	44	16.5	AAXL13282	Aaxl1282 Enterococ
12	44	16.5	AAS99077	Abs99077 Enterococ
13	44	16.5	ADEF77343_05	Continuation (6 of 16)
14	44	16.5	ADEF77343_07	Continuation (8 of 16)
15	44	16.5	ADEF77343_18	Continuation (19 of 24)
16	40	15.0	AABF61572	Aaf61572 L. casei
17	40	15.0	AABF61571	Aaf61571 L. casei
18	40	15.0	AABF61575	Aaf61575 Pediococc
19	40	15.0	AABF61574	Aaf61574 Pediococc
20	40	15.0	ABL154766	Ab154766 Pediococc
21	35	13.1	AAV79347	Aav79347 Staphyloc

c 95 35 13.1 15249 2 AAV74413
c 96 35 13.1 3046 2 AAV74367
c 97 34 12.7 400 2 AAV78250
c 98 31 11.6 213 2 AAV78941
c 99 30 11.2 239 2 AAV78891
c 100 30 11.2 628 2 AAV78162

Aav74413 Staphyloc
Aav74367 Staphyloc
Aav78250 Staphyloc
Aav78941 Staphyloc
Aav78891 Staphyloc
Aav78162 Staphyloc

RESULT 1
ID AAF61566
XX AAF61566 standard; DNA; 267 BP.
XX
XX
XX
XX
DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.
XX
KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
OS Lactobacillus brevis.
XX
PN DE19945964-A1.
XX
PD 05-APR-2001.
XX
PP 24-SEP-1999; 99DE-01045964.
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PR 24-SEP-1999; 99DE-01045964.
XX
PA (BIOT-) BIOTECN DIAGNOSTICS GMBH.
XX
PT Fandke M, Gasch A, Berghof K;
XX
DR WPI; 2001-246136/26.

ALIGNMENTS

QY

Db

QY

Db

QY

Db

QY

QY

RESULT 1
ID AAF61566
XX AAF61566 standard; DNA; 267 BP.
XX
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DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.
XX
KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
OS Lactobacillus brevis.
XX
PN DE19945964-A1.
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PD 05-APR-2001.
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PP 24-SEP-1999; 99DE-01045964.
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PR 24-SEP-1999; 99DE-01045964.
XX
PA (BIOT-) BIOTECN DIAGNOSTICS GMBH.
XX
PT Fandke M, Gasch A, Berghof K;
XX
DR WPI; 2001-246136/26.

RESULT 2

ID AAF61567
XX AAF61567 standard; DNA; 326 BP.

AC

AAF61567;
02-JUL-2001 (first entry)XX
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KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
OS Lactobacillus lindneri.
XX
PN DE19945964-A1.
XX
PD 05-APR-2001.
XX
PP 24-SEP-1999; 99DE-01045964.
XX
PR 24-SEP-1999; 99DE-01045964.
XX
PA (BIOT-) BIOTECN DIAGNOSTICS GMBH.
XX
PT Fandke M, Gasch A, Berghof K;
XX
DR WPI; 2001-246136/26.

RESULT 2

ID AAF61567
XX AAF61567 standard; DNA; 326 BP.

AC

AAF61567;
02-JUL-2001 (first entry)XX
DE Lactobacillus lindneri 23S rRNA-spacer-5S rRNA DNA fragment.XX
KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
OS Lactobacillus lindneri.
XX
PN DE19945964-A1.
XX
PD 05-APR-2001.
XX
PP 24-SEP-1999; 99DE-01045964.
XX
PR 24-SEP-1999; 99DE-01045964.
XX
PA (BIOT-) BIOTECN DIAGNOSTICS GMBH.
XX
PT Fandke M, Gasch A, Berghof K;
XX
DR WPI; 2001-246136/26.

XX
CC This invention describes a novel method for detecting microorganisms (A)
CC of importance in brewing which comprises treating a sample with at least
CC two primers (P1) that hybridize to a consensus region in the nucleic acid
CC of (A), at least part of the microbial nucleic acid is amplified, the
CC amplicon is treated with at least one probe (P2) that hybridizes
CC specifically with a sequence common to all (A) or specific for one or
CC more families, genera or species, and any formation of hybrids is
CC detected. The method is used to detect, identify and/or characterize
CC microorganisms in beer or brewing materials, particularly for detecting
CC contamination. The method may detect the entire range of contaminating
CC microbes, either as a general test for contamination or as a test
CC specific for particular genera or (sub)species. It is quicker than known
CC microbiological methods, and can detect several organisms in the same
CC sample, including organisms not presently recognized as contaminants. The
CC method provides an early indication of contamination and can be automated
CC for high throughput analysis
XX
SQ Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;
Query Match 100.0%; score 267; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.8e-131; Indels 0; Gaps 0;
Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATTTGGAGTAAGACCCCTGAGAGATCGGTAGATAGCTGGAGTACGCGCCG 60
1 TATATTGGAGTAAGACCCCTGAGAGATCGGTAGATAGCTGGAGTACGCGCCG 60
QY 61 TGAGGGTGAGGGGACCGAGTACTAATGGTCGAGGACTAACAACTCAACAGTAGT 120

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:16:19 ; Search time 1543.47 Seconds

Perfect score: 267

Sequence: 1 tataatggaaagtaagaccc...agtagttggggatcgcccc 267

Scoring table: Oligo-NUC

Word size: 10

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters: 32822875 seqs., 18219865908 residues

Post-processing: Listing first 100 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hrc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	56	21.0	793	8	BH2369094 Cct100.1.
2	22	8.2	3268	8	BH7710998 LIMGlaG72
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4	20	7.5	613	4	BT150715 BB17001A
5	20	7.5	693	8	BZ110405 CH230-3369
6	20	7.5	830	15	BZ076210 1Kf5d10.
7	19	7.1	547	8	BH386373 AG-ND-123
8	19	7.1	586	8	BH8223931 BACPP2-D0
9	19	7.1	657	2	AQ779183 HS-3185-A
10	19	7.1	672	8	BB865729 BB865729
11	19	7.1	692	8	BH396985 AG-ND-137
12	19	7.1	696	2	BB113195 UTR-BJ17
13	19	7.1	703	8	BH367775 AG-ND-137
14	19	7.1	709	8	BH402869 AG-ND-140
15	19	7.1	759	8	BH381344 AG-ND-180
16	19	7.1	800	5	BX811725 BX811725
17	19	7.1	829	8	A2540485 ENTDG39TF
18	19	7.1	877	8	CCL41525 NDL32K2.
19	19	7.1	888	8	CG995204 MBRMD88TP
20	19	7.1	889	1	AA815431 AA815431
21	18	6.7	161	1	AA815431 aa165a05.s
22	18	6.7	233	5	BO465654 BM76623 EBM76623
23	18	6.7	275	1	AV1515185 AV1515185
24	18	6.7	286	1	AV1515185 AV1515185

RESULT 1
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LOCUS BZ369094
DEFINITION Cot100.1.2.D04 Maize Cot100 library Zea mays genomic, genomic
VERSION BZ369094.1
KEYWORDS GSS
SOURCE Zea_mays
ORGANISM Zea mays
SPECIES Maize; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 793)
AUTHORS Yuan,Y., Samiguel,P. and Bennetzen,J.L.
TITLE High Cot sequence analysis of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Bennetzen JL
Department of Biological Sciences
Purdue University
Hansen 339#, Purdue University, West Lafayette, IN 47907, USA
Tel: 765 494 4919
Fax: 765 496 1496
Email: maize@libo.bio.purdue.edu
Forward and reverse reads were assembled when significant overlap
was detected.
Seq primer: T7 and T3
Class: shotgun
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/note="Organ: young leaves; Vector: pcr4TOPO; Maize
genomic DNA was Sheared to fragments averaging about 1.8
kb, was denatured and then reassociated in 1X SSC at
65°C. After a given Cot value was reached, aliquots were
run over a hydroxypatite (HAP) column in order to
separate single stranded DNA from double stranded DNA. The
single stranded DNA was then converted to a double
stranded form with one round of Klenow DNA Polymerase
treatment with random-mers primers. The double-stranded
fragments were then further size-selected over an agarose
gel and cloned into the PCR4 TOPO vector."
ORIGIN
Query Match 8.2%; Score 22; DB 8; Length 3268;
Best Local Similarity 100.0%; Pred. No. 0.51; Mismatches 0;
Matches 22; Conservative 0; Indels 0; Gaps 0;
Db 422 TGGAGCGGACCACTACTATCG 443
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BH771024
LOCUS BH771024
DEFINITION BH771024
VERSION BH771024.1
KEYWORDS GSS
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
Lactobacillales; Streptococcaceae;
Lactococcus.
REFERENCE Bolotin,A., Ehrlich,S.D. and Sorokin,A.
AUTHORS Studies of genomes of dairy bacteria Lactococcus lactis
TITLE Sci. Aliments (2002) In press
JOURNAL Genetique Microbiologie
COMMENT INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokin@jouy.inra.fr
best homologue in strain IL1403 is ywGA (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
FEATURES source
source
1. .6499
/organism="Lactococcus lactis subsp. cremoris"

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:16:19 ; Search time 115.616 Seconds

(without alignments)

6303.600 Million cell updates/sec

Title: US-10-088-666-74

Perfect score: 20

Sequence: 1 gagggagaagaatctttat 20

Scoring table: Oligo_NUC` Gapext 60.0 , Gapext 60.0

Searched: 3282875 seqs, 18229865908 residues

Word.size: 10

Total number of hits satisfying chosen parameters: 725526

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hcc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gns1:*
- 9: gb_gns2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	17	85.0	268	2	BB434970
C 3	17	85.0	295	4	BB434970
C 4	17	85.0	17	584	BB16700
C 5	17	85.0	696	2	BB113195
C 6	17	85.0	1025	9	BB42767
C 7	16	80.0	205	4	BB98912
C 8	16	80.0	262	8	BB471789
C 9	16	80.0	301	2	BB436559
C 10	16	80.0	409	1	AV540606
C 11	16	80.0	411	8	BB23273
C 12	16	80.0	419	6	CB774501
C 13	16	80.0	425	1	AA31772
C 14	16	80.0	425	8	AB860424
C 15	16	80.0	442	9	CB658098
C 16	16	80.0	445	6	CB744332
C 17	16	80.0	454	6	BBQ32471
C 18	16	80.0	467	6	CB714203
C 19	16	80.0	468	1	AL046182
C 20	16	80.0	520	9	CE571149
C 21	16	80.0	531	6	CA631367
C 22	16	80.0	542	4	BB249708
C 23	16	80.0	573	9	CE251105
C 24	16	80.0	575	2	BF483725

c 25 16 80.0 581 8 A2982290 2M0263J04

c 26 16 80.0 590 4 BM04665 3N704665 UT-E-CII-

c 27 16 80.0 595 6 CB177815 i-21c01.x

c 28 16 80.0 607 4 BJ567993 BJ567993

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c 30 16 80.0 620 5 BX254803 BX254803

c 31 16 80.0 635 8 A2884762 IM014224

c 32 16 80.0 650 4 BI113486 6D2899335

c 33 16 80.0 658 7 CN305165 17004250

c 34 16 80.0 662 5 BQ829603 E0829603 LI61n2145

c 35 16 80.0 671 6 CB840482 CB840482 M15E-0781

c 36 16 80.0 674 5 BX18105 BX918105

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c 39 16 80.0 730 8 A2342561 AG42832 MUS

c 40 16 80.0 737 9 AG42832 MUS

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VERSION	BB4345272 BB435272			
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Apis mellifera				
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Rhamnoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis;				
1 (bases 1 to 613)				
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L., Pardinas, J., Robertson, H.M., Soares, B. and Robinson, G.E.				
Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee				
Genome Res. 12 (4), 555-566 (2002)				
MEDLINE				
PUBMED				
COMMENT				
Contact: Gene E. Robinson				
Department of Entomology				
University of Illinois				
505 S. Goodwin Ave., Urbana, IL 61801, USA				
Tel: 217 265 0309				
Fax: 217 265 3499				
Email: generobi@life.uiuc.edu				
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.				
PCR PRIMERS				
FORWARD: TATTCGACTCACTATAGG				
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ORIGIN				
Query Match 95.0%; Score 19; DB 4; Length 613;				
Best Local Similarity 100.0%; Pred. No. 6.4; O; Indels 0; Gaps 0; Mismatches 19; Conservative 0;				
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VERSION	BB434970			
ACCESSION	BB434970.1 GI:9274697			
KEYWORDS	EST			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
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Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 268)			
AUTHORS	Konno,H., Alzawa,K., Akahira,S., Akivama,J., Arakawa,T.,			
Carminci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,				
Hirayama,T., Hori,F., Ishii,Y., Ishikawa,J., Ichikawa,T., Itou,M.,				
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,				
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C.,				
Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H.,				
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Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T.,				
Sobabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A.,				
Takahashi,F., Tominaga,N., Toya,T., Tunoda,Y., Watanuki,A.,				
Watanabe,S., Yamamuro,T., Yamamoto,I., Yano,R., Yasunishi,A.,				
Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.				
RIKEN Mouse ESTs (Konno,H., et al.)				
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Yoshinide Hayashizaki			
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OM nucleic - nucleic search, using sw model		
Run on:	November 15, 2004, 14:28:49 ; Search time 34.4144 Seconds	(without alignments)
	US-10-088-666-74	3138.794 Million cell updates/sec
Title:	Perfect score: 20	US-10-425-114-12489
Sequence:	1 gggggaaagaatcttcatat 20	US-10-425-115-144409
Scoring table:	ORIGO-NUC , Gapext 60.0 , Gapext 60.0	Sequence 34049, AP
Searched:	3625171 seqs, 2700493622 residues	Sequence 9722, AP
Word-size:	10^1	Sequence 9722, AP
Total number of hits satisfying chosen parameters:	95006	Sequence 4989, AP
Minimum DB seq length:	0	Sequence 139, AP
Maximum DB seq length:	200000000	Sequence 52109, A
Post-processing: Listing first 100 summaries		Sequence 3223, A
Database :	Published Applications NA:*	Sequence 43260, A
1: /cggn2_6/prodata2/pupnna/us07_pubcomb.seq:*	c	Sequence 11, APPL
2: /cggn2_6/prodata2/pupnna/us07_pubcomb.seq:*	c	Sequence 7, APPL
3: /cggn2_6/prodata2/pupnna/us07_pubcomb.seq:*	c	Sequence 3, APPL
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7: /cggn2_6/prodata2/pupnna/us08_pubcomb.seq:*	c	Sequence 10, APPL
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9: /cggn2_6/prodata2/pupnna/us09_pubcomb.seq:*	c	Sequence 6, APPL
10: /cggn2_6/prodata2/pupnna/us09_pubcomb.seq:*	c	Sequence 21, APPL
11: /cggn2_6/prodata2/pupnna/us09c_pubcomb.seq:*	c	Sequence 36, APPL
12: /cggn2_6/prodata2/pupnna/us09_pubcomb.seq:*	c	Sequence 32, APPL
13: /cggn2_6/prodata2/pupnna/us10_pubcomb.seq:*	c	Sequence 31, APPL
14: /cggn2_6/prodata2/pupnna/us10_pubcomb.seq:*	c	Sequence 30, APPL
15: /cggn2_6/prodata2/pupnna/us10c_pubcomb.seq:*	c	Sequence 29, APPL
16: /cggn2_6/prodata2/pupnna/us10d_pubcomb.seq:*	c	Sequence 35, APPL
17: /cggn2_6/prodata2/pupnna/us10e_pubcomb.seq:*	c	Sequence 34, APPL
18: /cggn2_6/prodata2/pupnna/us11_pubcomb.seq:*	c	Sequence 33, APPL
19: /cggn2_6/prodata2/pupnna/us11_pubcomb.seq:*	c	Sequence 32, APPL
20: /cggn2_6/prodata2/pupnna/us11c_pubcomb.seq:*	c	Sequence 31, APPL
21: /cggn2_6/prodata2/pupnna/us60_pubcomb.seq:*	c	Sequence 30, APPL
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	95006	Sequence 28, APPL
SUMMARIES		Sequence 41, APPL
Result No.	Score	Sequence 42, APPL
No.	Match Length DB ID	Sequence 43, APPL
	Description	Sequence 44, APPL
1	18 90.0 465 18 US-10-425-115-15008	Sequence 434, APPL
2	17 85.0 127767 17 US-10-322-381-797	Sequence 434, APPL
3	16 80.0 688 13 US-10-027-332-102170	Sequence 434, APPL
4	16 80.0 688 15 US-10-027-532-102171	Sequence 434, APPL
5	16 80.0 688 15 US-10-027-532-102170	Sequence 434, APPL
6	16 80.0 688 15 US-10-027-532-102171	Sequence 434, APPL
7	16 80.0 2022 17 US-10-437-563-57769	Sequence 434, APPL
8	16 80.0 6109 10 US-09-795-661-1	Sequence 434, APPL
9	16 80.0 6200 10 US-09-795-661-3	Sequence 434, APPL
10	16 80.0 6327 15 US-10-369-693-28224	Sequence 434, APPL
11	16 80.0 218155 13 US-10-087-92-400	Sequence 434, APPL
12	15 75.0 255 15 US-10-149-736-7	Sequence 434, APPL
13	15 75.0 448 16 US-10-425-114-12489	Sequence 12489, A
14	15 75.0 448 18 US-10-425-115-144409	Sequence 140409, A
15	15 75.0 539 10 US-09-814-353-3104	Sequence 34049, A
16	15 75.0 539 10 US-09-814-353-3104	Sequence 34049, A
17	15 75.0 571 14 US-10-319-220-247	Sequence 9722, AP
18	15 75.0 605 9 US-09-958-8428-4959	Sequence 247, AP
19	15 75.0 605 11 US-09-938-842A-4989	Sequence 4989, AP
20	15 75.0 1166 14 US-10-319-220-1399	Sequence 139, AP
21	15 75.0 1284 17 US-10-437-963-52109	Sequence 52109, A
22	15 75.0 1286 17 US-10-437-963-3223	Sequence 3223, A
23	15 75.0 1323 16 US-10-424-559-42260	Sequence 43260, A
24	15 75.0 1340 10 US-09-845-416-11	Sequence 11, APPL
25	15 75.0 1657 10 US-09-845-416-7	Sequence 7, APPL
26	15 75.0 1991 10 US-09-845-416-3	Sequence 3, APPL
27	15 75.0 2046 17 US-10-667-034-8	Sequence 2, APPL
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32	15 75.0 3999 10 US-09-845-416-6	Sequence 6, APPL
33	15 75.0 4182 10 US-09-845-416-2	Sequence 21, APPL
34	15 75.0 4414 10 US-09-845-416-32	Sequence 36, APPL
35	15 75.0 4476 10 US-09-845-416-31	Sequence 32, APPL
36	15 75.0 4498 10 US-09-845-416-30	Sequence 30, APPL
37	15 75.0 4825 10 US-09-845-416-29	Sequence 29, APPL
38	15 75.0 4848 10 US-09-845-416-35	Sequence 27, APPL
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40	15 75.0 4990 10 US-09-845-416-34	Sequence 23, APPL
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43	15 75.0 5339 15 US-10-149-736-40	Sequence 17, APPL
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62	15 75.0 175561 16 US-10-289-662-1	Sequence 1, APPL
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 C 87 14 70.0 436 16 US-10-424-539-7234
 C 88 14 70.0 498 9 US-09-783-590-6201
 C 89 14 70.0 544 16 Sequence 6021, AP
 C 90 14 70.0 569 13 Sequence 15, AP
 C 91 14 70.0 575 15 Sequence 129, AP
 C 92 14 70.0 579 15 Sequence 129, AP
 C 93 14 70.0 599 9 Sequence 82, AP
 C 94 14 70.0 599 13 Sequence 129, AP
 C 95 14 70.0 599 15 Sequence 129, AP
 C 96 14 70.0 611 13 Sequence 129, AP
 C 97 14 70.0 611 13 Sequence 129, AP
 C 98 14 70.0 611 15 Sequence 129, AP
 C 99 14 70.0 611 15 Sequence 129, AP
 100 14 70.0 615 16 Sequence 129, AP

ALIGNMENTS

RESULT 1
US-10-425-115-45008

; Sequence 45008, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovacic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(522)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 45008

; LENGTH: 465

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE: OTHER INFORMATION: Clone ID: MRT4577_141051C.1

; US-10-425-115-45008

Query Match 90.0%; Score 18; DB 18; Length 465;

Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGAGAGAGTCTTAT 20

Db 439 GGAGAGAGTCTTAT 456

RESULT 2
US-10-322-281-797

; Sequence 797, Application US/10322281

; Publication No. US20040126762A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc S. Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001000

; CURRENT APPLICATION NUMBER: US/10/322,281

; CURRENT FILING DATE: 2002-12-17

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 797
 ; LENGTH: 127767

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE: misc_feature

; LOCATION: (1)..(127767)

; OTHER INFORMATION: n = A,T,C or G

Sequence 316408, Sequence 79234, A
 Sequence 6021, AP
 Sequence 15, AP
 Sequence 129, AP
 Sequence 129, AP
 Sequence 82, AP
 Sequence 129, AP
 Sequence 6356, A
 Sequence 6356, A
 Sequence 221890,
 Sequence 297152,
 Sequence 221890,
 Sequence 297152,
 Sequence 18935, AUS-10-322-281-797
 ; Query Match 85.0%; Score 17; DB 17; Length 127767;
 ; Best Local Similarity 100.0%; Pred. No. 4.3; 0; MisMatches 17; Conservative 0; Indels 0; Gaps 0;; QY 4 GGAGAGAGTCTTAT 20
 ; DB 5129 GGAGAGAGTCTTAT 5145
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 103827.129; CURRENT APPLICATION NUMBER: US/10/027-632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/167,363
 ; PRIOR FILING DATE: 2000-04-20
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR FILING DATE: 1999-11-23
 ; PRIOR APPLICATION NUMBER: US 60/156,358
 ; PRIOR FILING DATE: 1999-09-28
 ; PRIOR APPLICATION NUMBER: US 60/146,002
 ; PRIOR FILING DATE: 1999-08-09
 ; NUMBER OF SEQ ID NOS: 325720
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 102170
 ; LENGTH: 688
 ; TYPE: DNA
 ; ORGANISM: Human; US-10-027-632-102170
 ; Query Match 90.0%; Score 16; DB 13; Length 688;
 ; Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;; QY 2 AGGGAGAGTCT 17
 ; DB 631 AGGGAGAGTCT 616; RESULT 4
US-10-027-632-102171/C
 ; Sequence 102171, Application US/10027632
 ; Publication No. US20020198371A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, David G.
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 ; FILE REFERENCE: 108927..129
 ; CURRENT APPLICATION NUMBER: US/10/027-632
 ; CURRENT FILING DATE: 2002-04-30
 ; PRIOR APPLICATION NUMBER: US 60/218,006
 ; PRIOR FILING DATE: 2000-07-12
 ; PRIOR APPLICATION NUMBER: US 60/198,676
 ; PRIOR APPLICATION NUMBER: US 60/193,483
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: US 60/185,218
 ; PRIOR FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/167,363

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29	13	65.0	196	4	US-09-513-998C-27882
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53	13	65.0	470	3	US-09-124-523-77
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58	13	65.0	631	4	US-09-270-767-10321
59	13	65.0	786	2	US-09-228-312-2137
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62	13	65.0	844	3	US-08-988-416-292
63	13	65.0	877	4	US-09-270-767-14474
64	13	65.0	885	4	US-09-583-110-1634
65	13	65.0	948	4	US-09-210-767-11984
66	13	65.0	971	3	US-09-248-335-65
67	13	65.0	1001	4	US-10-170-097-312
68	13	65.0	1001	4	US-10-170-097-312
69	13	65.0	1008	4	US-09-940-241-348
70	13	65.0	1020	4	US-09-107-522-2766
71	13	65.0	1100	4	US-09-270-767-14335
72	13	65.0	1200	4	US-09-543-682A-761
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ALIGNMENTS

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US-09-795-061-1

; Sequence 1, Application US/09795061

; Patent No. 6759528

; GENERAL INFORMATION:

; APPLICANT: Greenspan, Daniel S

; TITLE OF INVENTION: Compositions affecting programmed cell

; TITLE OF INVENTION: death and their use in the modification of forestry plant develop-

; FILE REFERENCE: 1_022

; CURRENT APPLICATION NUMBER: US/09/325,932A

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 205

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 139

; LENGTH: 1166

; TYPE: DNA

; ORGANISM: Pinus radiata

; US-09-325-932A-139

; Query Match

; Best Local Similarity 100.0%; Pred. No. 2.4;

; Matches 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 1 GAGGGAGAGTCTC 16

; Db 4907 GAGGGAGAGTCTC 4922

; RESULT 2

US-09-795-061-3

; Sequence 3, Application US/09795061

; Patent No. 6759528

; GENERAL INFORMATION:

; APPLICANT: Greenspan, Daniel S

; TITLE OF INVENTION: Pro-Alpha 3 (V) Collagen Genes

; FILE REFERENCE: 96-0295-96781

; CURRENT APPLICATION NUMBER: US/09/795, 061

; CURRENT FILING DATE: 2001-02-26

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 3

; LENGTH: 6109

; TYPE: DNA

; ORGANISM: Mus musculus

; FEATURE: CDS

; NAME/KEY: CDS

; LOCATION: (82)..(5298)

; US-09-795-061-1

; RESULT 3

US-09-325-932A-139/c

; Sequence 139, Application US/09325932A

; Patent No. 651604

; GENERAL INFORMATION:

; APPLICANT: Flinn, Barry

; APPLICANT: Iasham, Annette

; TITLE OF INVENTION: Compositions affecting programmed cell

; TITLE OF INVENTION: death and their use in the modification of forestry plant develop-

; FILE REFERENCE: 1_022

; CURRENT APPLICATION NUMBER: US/09/325,932A

; CURRENT FILING DATE: 1999-06-04

; NUMBER OF SEQ ID NOS: 205

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 139

; LENGTH: 1166

; TYPE: DNA

; ORGANISM: Pinus radiata

; US-09-687-875A-1/c

; Sequence 1, Application US/09687875A

; Patent No. 6547786

; GENERAL INFORMATION:

; APPLICANT: Xiao, Xiao

; TITLE OF INVENTION: METHOD AND VECTOR FOR PRODUCING AND TRANSFERRING TRANS-SPliced PPI

; CURRENT APPLICATION NUMBER: US/09/687, 875A

; CURRENT FILING DATE: 2000-01-13

; PRIOR FILING DATE: 1999-10-15

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 1

; LENGTH: 5952

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: CDS

; NAME/KEY: misc feature

; LOCATION: (2897)..(2898)

; OTHER INFORMATION: S4 junction site

; NAME/KEY: misc feature

; LOCATION: (3198)..(3199)

; OTHER INFORMATION: S2 junction site

; US-09-687-875A-1

; Query Match

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; Matches 0; Mismatches 0; Indels 0; Gaps 0;

; Qy 3 GGGAGAGTCTC 17

; Db 874 GGGAGAGTCTC 8760

; RESULT 5

US-09-484-970B-50/c

; Sequence 60, Application US/09484970B

; Patent No. 6420186

; GENERAL INFORMATION:

; APPLICANT: Jones, Karen A.

; TITLE OF INVENTION: Walker, Michael G.

; FILE REFERENCE: PP-0014 US

; CURRENT APPLICATION NUMBER: US/09/484, 970B

; CURRENT FILING DATE: 2000-01-18

; NUMBER OF SEQ ID NOS: 172

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GenCore version 5.1.6

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SUMMARIES

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59	c	15	75.0	13957	6	ABR81959	Abk81959 cDNA enco
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75	c	15	75.0	273254	3	AR81914	Acr81914 Chlamydia
76	c	15	75.0	273254	3	ACT16287	Act16287 Human mic
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78	c	15	75.0	72	3	ACD48437	Acd48437 Arabidops
79	c	15	75.0	175561	12	ADT44398	Adt44398 Plant CDN
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85	c	15	75.0	333	12	ADT44398	Adt44398 Plant CDN
86	c	15	75.0	483	4	AMH6218	Ahm6218 Human CDN
87	c	15	75.0	569	1	ABP88761	Abp88761 EST clone
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91	c	15	75.0	615	8	ACM31065	Acm31065 Prokaryot
92	c	15	75.0	636	3	ADM0357	Aaf0357 Fusaria
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Page
2

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AC07683	Mus muscul
AC051634	Oryza sat
AC059348	Homo sapi
AL071795	Mouse DNA
AC15887	Mus muscul
AP003574	Oryza sat
AC15945	Homo sapi
All12193	Human DNA
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AC173793	Homo sapi
AC14149	Homo sapi
AC053784	Homo sapi
AC051631	Homo sapi
AC006075	Homo sapi
AC04371	Homo sapi
AP004992	Oryza sat
AC079079	Homo sapi
AC112217	Rattus no
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AC056840	Homo sapi
AL255707	Human DNA
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AC146318	Gallus ga
AL141942	Arabidops
AL163546	Arabidops
AC009570	Homo sapi
ACT8816	Mus muscul
AC140931	Mus muscul
297343	Arabidopsis
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AC138335	Mus muscul
AC154506	Gallus ga
AC079454	Mus muscul
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AY178284	Grassland
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AF657545	Unculture
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AY043418	Arabidops
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CQ02651	Sequence
AX102954	Unculture
AX102954	Sequence

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LOCUS AX105802 Sequence 74 from Patent WO0123605.

DEFINITION Sequence 74 from Patent WO0123605.

ACCESSION AX105802

VERSION AX105802.1 GI:13921815

KEYWORDS

- synthetic construct
- artificial sequences.

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS Fandke, M., Gasch, A. and Berghof, K.

TITLE Method and nucleic acids for determining the presence of micro-organisms specific to the brewing process

JOURNAL Patent: WO 0123605-A 74 05-APR-2001; Biotecon Diagnostics GmbH (DE)

FEATURES Location/Qualifiers

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- /organism="unassigned DNA"
- /db_xref=taxon:3260" /note="spezifische Sequenz fur Lactobacillus brevis"

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Db 1 GAGGGAGAGTCTCTTAT 20

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LOCUS AX105729 Sequence 1 from Patent WO0123605.

DEFINITION Sequence 1 from Patent WO0123605.

ACCESSION AX105729

VERSION AX105729.1 GI:13921742

KEYWORDS

- Lactobacillus brevis

SOURCE

ORGANISM Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.

REFERENCE

AUTHORS Fandke, M., Gasch, A. and Berghof, K.

TITLE Method and nucleic acids for determining the presence of micro-organisms specific to the brewing process

JOURNAL Patent: WO 0123605-A 10-APR-2001; Biotecon Diagnostics GmbH (DE)

FEATURES Location/Qualifiers

- source 1..267
- /organism="Lactobacillus brevis"
- /mol_type="unassigned DNA"
- /db_xref=taxon:1580" /note="unassigned DNA"

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Qy 1 GAGGGAGAGTCTCTTAT 20

Db 1 GAGGGAGAGTCTCTTAT 20

ALIGNMENTS

AC117613/C AC117613 249813 bp DNA linear HTG 25-MAR-2004

LOCUS AC117613 Mus musculus chromosome 6 clone RP23-106C18 map 6, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.

DEFINITION Mus musculus chromosome 6 clone RP23-106C18 map 6, *** SEQUENCING IN PROGRESS ***, 9 unordered pieces.

ACCESSION AC117613

VERSION AC117613.6 GI:4576872

REFERENCE

AUTHORS Birren, B., Nusbaum, C. and Lander, E.

SOURCE

ORGANISM Mus musculus (house mouse)

REFERENCE

AUTHORS Birren, B., Nusbaum, C. and Lander, E.

TITLE Mus musculus chromosome 6, clone RP23-106C18

JOURNAL Unpublished

2 (bases 1 to 229813)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukaghter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearallino, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, J., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karakas, A., Keils, C., Larocque, K., Lamazares, R., Landers, T., Lehozicky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McErlean, K., Nedim, J., Menau, L., Mihowa, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicoll, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Pollard, V., Raymond, C., Repta, R., Rieback, M., Riley, R., Rose, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolarovic, N., Straus, N., Subramanian, A., Talamas, J., Testayre, S., Theodore, J., Topham, K., Travers, M., Travis, N., Tridilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.-J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (10-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 229813)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Archichi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukaghter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagon, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Keils, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menau, L., Mihowa, T., Mlenga, V., Murphy, T., Nayor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunthang, P., Pierre, N., Ramasamy, U., Raymond, C., Rettig, R., Rose, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfave, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Verkarakaran, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL Direct Submission

Submitted (25-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:16:19 ; Search time 144.52 Seconds
(without alignments)
6303.600 Million cell updates/sec

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Scoring table: Oligo_Nuc.. Gapop 60.0 , Gapext 60.0

Searched: 3282875 seqs, 18219865908 residues

Word_size: 10 ~

Total number of hits satisfying chosen parameters: 675855

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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 3: gb_hcc:
 4: gb_est3:
 5: gb_est4:
 6: gb_est5:
 7: gb_est6:
 8: gb_gns1:
 9: gb_gns2:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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17	17	68.0	513	9 CSE78285	
18	17	68.0	519	9 C2256503	
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20	17	68.0	535	8 BR829578 BACP3-MI	
C	21	17	68.0	544	4 BR1467380
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	REFERENCE
RESULT 1	1. (bases 1 to 888), Town,C.D., Shetty,J., Koo,H. and Feldblum,T.F. Sequencing of BAC ends from <i>Medicago truncatula</i>
CC141515	AU03197 AU03197 BI356911 RE43196.5
LOCUS	CC141515 877 bp DNA linear GSS 16-APR-2003
DEFINITION	NDL_32K2_SP6 Notre Dame Liverpool <i>Aedes aegypti</i> genomic clone.
ACCESSION	NCBI32K2_ genomic survey sequence.
VERSION	CC141515.1 GI:30010570
KEYWORDS	GSS; <i>Aedes aegypti</i> (yellow fever mosquito)
SOURCE	<i>Aedes aegypti</i> (yellow fever mosquito)
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Nematocera; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; <i>Aedes</i> ; Stegomyia.
COMMENT	1. (bases 1 to 877) Other_GSS: NDL_32K2_T7 Contact: Brendan Loftus Department of Eukaryotic Genomics
AUTHORS	Lofrus,B., Shetty,J., Knudson,D. and Severson,D.
TITLE	TIGR Unpublished (2003)
JOURNAL	
FEATURES	Location/Qualifiers
source	1. .888 'organism="Medicago truncatula"' 'mol_type="genomic DNA"' 'cultivar="genotype A17"' 'db_xref=taxon:3880' 'clone="84P8"' 'clone_lib="mtb12"' 'note="Vector: pBelBAC1; Site_1: HindIII; Site_2: HindIII; Cook, D.R. and Kim, D.J., unpublished"'
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source	Best local Similarity 100.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0; Matches 19; Conservative 0;
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CR86805	CR286805 CR286805 Oryza sativa library (Han B) mRNA Linear EST 27-FEB-2004
DEFINITION	CR286805 mRNA sequence.
ACCESSION	CR286805
VERSION	CR286805.1 GI:44673371
KEYWORDS	EST.
SOURCE	Oryza sativa
ORGANISM	Bikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE	1. (bases 1 to 668) Han,B., Feng,Q., Huang,Y.C., Ying,K., Li,Y., Guan,J.P., Zhu,J.J., Zhao,Q.J., Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Wang,Q.J., Zhang,L., Lu,Y., Li,T., Zhang,Y., Hu,H., Jia,P.X., Zhang,Y.J., Lu,Y., Li,C., Li,T., Zhang,Y., Wu,S.A. and Xue,Y.B.
AUTHORS	Zhang,L., Lan,L.F., Chen,W., Wu,S.A. and Xue,Y.B.
TITLE	Rice cDNA EST clone
JOURNAL	
COMMENT	Unpublished (2003)
ORIGIN	Contact: Han Bin
FEATURES	National Center for Gene Research
source	Chinese Academy of Sciences 500# Cao Bao Road, Shanghai 200233, China
Db	
RESULT 2	
CG965204	CG965204 888 bp DNA Linear GSS 15-DEC-2003
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DEFINITION	Survey sequence.
ACCESSION	CG965204
VERSION	CG965204.1 GI:39890624
KEYWORDS	GSS.
SOURCE	<i>Medicago truncatula</i> (barrel medic)
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
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ORIGIN	Query Match
COMMENT	72.0%; Score 18; DB 7; Length 668;

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:28:49 ; Search time 43.018 Seconds
(Without alignments)
338,794 Million cell updates/sec

Title: US-10-088-666-73
Perfect score: 25
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Searched: 3625171 seqs, 2700493622 residues
Word_size: 10 ^

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 16	16	949	US-10-027-632-122128	Sequence 122128,
c 17	16	950	US-10-027-632-254585	Sequence 254585,
c 18	16	950	US-10-027-632-254585	Sequence 254585,
c 19	16	2052	US-10-027-632-257250	Sequence 257250,
c 20	16	2052	US-10-027-632-257250	Sequence 257250,
c 21	16	64.0	US-10-282-122A-31273	Sequence 21490, A
c 22	16	64.0	US-10-282-122A-31273	Sequence 21490, A
c 23	16	64.0	US-10-356-631-3	Sequence 3, Appli
c 24	16	64.0	US-10-311-655-758	Sequence 758, APP
c 25	16	8979	US-10-221-613-138	Sequence 138, APP
c 26	16	38645	US-10-085-117-193	Sequence 193, APP
c 27	16	78695	US-10-719-370A-257	Sequence 257, APP
c 28	16	64.0	US-10-060-902-1	Sequence 1, Appli
c 29	16	64.0	322101	Sequence 1, Appli
c 30	16	64.0	367778	Sequence 1, Appli
c 31	15	60.0	449	US-10-312-811-1
c 32	15	60.0	220	US-10-242-35A-9107
c 33	15	60.0	466	US-10-027-632-40912
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c 71	15	60.0	854	US-09-903-190-67
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c 74	15	60.0	856	US-10-027-632-159755
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c 85	15	60.0	872	US-10-027-632-159755

RESULT 1
US-09-070-927A-714/c
; Sequence 714, Application US/09070927A
; Patent No. US2002012016A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunisch
; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/045,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 714:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1190 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 714:
; US-09-070-927A-714
Query Match 72.0%; Score 18; DB 9; Length 1190;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

RESULT 2
US-10-437-363-45894/c
; Sequence 45894, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; Kovacic, David K.
; Zhou, Yihua
; Cao, Yongwei
; Wu, Wei
; Boukharov, Andrey A.
; Li, Ping
; APPLICANT: Barbakau, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; Title of Invention: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45894
; LENGTH: 1891
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT4530_48814C.1
; US-10-437-963-45894

RESULT 3
US-10-311-455-1259
; Sequence 1259, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: Olik, Alexander
; Applicant: PIEPERBROCK, Christian
; Applicant: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determination of Cytosine Methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529,7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826,1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1259
; LENGTH: 5962
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 5264
; OTHER INFORMATION: n is a or g or c or t
; US-10-311-455-1259

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:18:54 ; Search time 10 6607 Seconds
 (without alignments)

1666.850 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25

Sequence: OmgO-NUC--

Scoring table: Gapop 60.0 ; Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word-size: 10

Total number of hits satisfying chosen parameters: 12495

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : issued Parents NA:*

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- 2: //cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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- 5: //cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: //cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query	Length	DB ID	Description
1	16	64.0	183	4	US-09-270-767-27323
2	16	64.0	442	4	US-09-270-767-11703
3	16	64.0	1275	4	US-09-248-796A-3319
4	16	64.0	6527	4	US-09-492-308A-3
5	15	60.0	285	4	US-09-248-796A-1887
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7	15	60.0	495	4	US-09-621-976-1493
8	15	60.0	572	4	US-09-593-360B-65
9	15	60.0	854	3	US-09-247-153-4
10	15	60.0	3001	4	US-09-559-33D-187
11	15	60.0	3552	4	US-09-107-532A-3026
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21	14	56.0	417	4	US-09-543-681A-643
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24	14	56.0	623	4	US-09-270-767-1516
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27	14	56.0	759	4	US-09-710-279-1031

SUMMARIES

Copyright (c) 1993 - 2004	GenCore version 5.1.6	Compugen Ltd.
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5: gb_ov;*	c	c
6: gb_pac;*	c	c
7: gb_pn;*	c	c
8: gb_pl;*	c	c
9: gb_pc;*	c	c
10: gb_ro;*	c	c
11: gb_sts;*	c	c
12: gb_sy;*	c	c
13: gb_un;*	c	c
14: gb_vl;*	c	c
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES		
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LOCUS	AX105801	Sequence 73 from Patent WO0123605.	25 bp	DNA	linear	PAT 30-APR-2001
DEFINITION						
VERSION	AX105801.1	GI:113921814				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		artificial Sequences.				
FEATURES						
REFERENCE						
AUTHORS		Fandie, M., Gasch, A. and Berghof, K.				
TITLE		Method and nucleic acids for determining the presence of				
micro-organisms specific to the brewing process						
JOURNAL		Patent: WO 0123605-A 73-05-APR-2001;				
Bioteccon Diagnostics GmbH (DE)						
Location/Qualifiers						
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		Matches 25; Conservative	0; Indels 0; Gaps 0;			
Qy						
Db						
RESULT 3						
AC079132/c						
LOCUS	AC079132	Homo sapiens chromosome 8 clone RP1-214J7 map 8,	64701 bp	DNA	linear	HTG 23-FEB-2001
DEFINITION						
VERSION	AC079132	HTG; HTGS_PHASE0.				
KEYWORDS						
ORGANISM	Homo sapiens	(human)				
REFERENCE						
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;				
TITLE		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
JOURNAL		1 (bases 1 to 6701)				
		Birren,B., Linton,L., Nusbaum,C. and Lander,E.				
REFERENCE		Unpublished				
AUTHORS		2 (bases 1 to 64701)				
		Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,				
		Anderson,S., Barna,N., Bartkiewicz,V., Beda,F., Boguslavskiy,L.,				
		Baukhalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,				
		Chopeley,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,				
		DeArbelaino,K., Deward,K., Diaz,J.S., Dodge,S., Ferreira,P.,				
		FritzHugh,W., Gade,D., Gallegos,J., Gardyna,S., Ginde,S., Goyette,M.,				
		Graham,I., Grand-Pierre,N., Hages,B., Haiford,A., Horton,L.,				
		Iliev,I., Johnson,R., Jones,C., Kahn,L., Karatas,A., Larocque,K.,				
		Lamazares,R., Landers,T., Leboeuf,C., Levine,R., Lieu,C., Liu,G.,				
		Macdonald,P., Margolis,N., McCarthy,M., McEwan,P., McKernan,K.,				
		McHeevers,R., McEdrin,J., Mendez,L., Milova,T., Mlenov,V.,				
		Morrow,J., Murphy,T., Naviar,J., Norman,C.H., O'Connor,T.,				
		O'Donnell,P., O'Neil,D., Oliver,T.M., Oliver,J., Peterson,K.,				
		Pierre,N., Pisani,C., Polkara,V., Raymond,C., Riback,M., Riley,R.,				
		Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,P.,				
		Sougnex,C., Spencer,B., Strange-Thomann,N., Stojanovic,N.,				
		Strauss,N., Subramanian,A., Talama,J.J., Tesfaye,S., Theodore,J.,				
		Turrell,A., Travers,M., Trigilio,J., Vassiliev,H., Vie,R., Vo,A.,				
		Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,				
		Zimmer,A. and Zody,M.				
TITLE		Direct Submission				
JOURNAL		Submitted (19-Aug-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA				
COMMENT		On Feb 23, 2001 this sequence version replaced gi:9857544.				
		All repeats were identified using RepeatMasker:				
		http://ftp.genome.washington.edu/RM/RepeatMasker.html				
		----- Project Information				
		Center project name: Bl0419				
		Center clone name: 214_J_7				

		* NOTE: This record contains 81 individual				
		* sequencing reads that have not been assembled into				
		* contigs. Runs of N are used to separate the reads				
		* and the order in which they appear is completely				
		* arbitrary. Low-pass sequence sampling is useful for				
		* identifying clones that may be gene-rich and allows				
		* overlap relationships among clones to be deduced.				
		* However, it should not be assumed that this clone				
		* will be sequenced to completion. In the event that				
		* the record is updated, the accession number will				
		* be preserved.				
		* 1 661: contig of 661 bp in length				
		* 662 761: gap of 100 bp				
		* 762 1473: contig of 712 bp in length				

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:16:19 ; Search time 121.396 Seconds (without alignments)

Scoring table: Oritco-NUC.., Gapop_60.0 , Gapext 60.0

Searched: 32822875 seqs., 18219865908 residues

Word size: 10

Total number of hits satisfying chosen parameters: 249193

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : EST:*

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2: gb_est2:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
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6	16	76.2	544	CG467735
7	16	76.2	588	BH2294116
8	16	76.2	648	CG30774
9	16	76.2	674	CG307783
10	16	76.2	682	BW213486
11	16	76.2	702	BH179655
12	16	76.2	9	CNS07107
13	16	76.2	709	BH226500
14	16	76.2	789	CG883248
15	16	76.2	9	CG901933
16	16	75.2	830	BZ076210
17	16	76.2	894	CG044759
18	16	76.2	9	CG044756
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RESULT 1
BH542735
LOCUS BOGXU95TR BOGX *Brassica oleracea* genomic clone BOGXU95, genomic
DEFINITION survey sequence.

ACCESSION BH542735.1
VERSION GI:17794516
SOURCE GSS.
ORGANISM *Brassica oleracea*

REFERENCE
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of *Brassica oleracea*.
JOURNAL Unpublished (2001)
COMMENT Other GSS: BOGXU95TR

TIGR
Contact: Chris Town
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: ctown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
Source

ORIGIN

1. .779
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="NOL00DH3"
/db_xref="taxon:3712"
/clone="BOGXU95"
/clone_id="BOGX"
/note="Vector: phos1; site_1: BstXI; 2-3 kb sheared genomic DNA inserted into phos1 using BstXI linkers."

RESULT 2
BUT225601/c
LOCUS BU225601 mRNA linear EST 26-NOV-2002
DEFINITION 727 bp mRNA clone CHEST295n19 5', mRNA sequence.

ACCESSION BU225601
VERSION GR:25451670
KEYWORDS
VERSION EST.
SOURCE Gallus gallus (chicken)
ORGANISM *Gallus gallus* (chicken)

REFERENCE
AUTHORS Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus;
 (bases 1 to 727).
Boardman,P.E., Sainz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs

ALIGNMENTS

RESULT 1
CBS590496 tigr-GSS-CBS590496
LOCUS AA771342 SWTBADAO0
DEFINITION CO750077 KBrrAB004P

ACCESSION BOGXU95TR BOGX *Brassica oleracea* genomic clone BOGXU95, genomic
VERSION GSS.
SOURCE GSS.
ORGANISM *Brassica oleracea*

REFERENCE
AUTHORS Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of *Brassica oleracea*.
JOURNAL Unpublished (2001)
COMMENT Other GSS: BOGXU95TR

TIGR
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 89, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 0161236009
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
 1. .727
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST295n19"
/dev_stage="22"
/lab_host="DH10B"
/clone_id="CSROCHM23"
/note="Organ: head; Vector: Bluescript II KS(+); Site_1: EcoRI; Site 2: NotI. This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adaptors, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the Bluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9220-9232 and Bonaldo et al., Genome Research 6 (1996) 91: 791, except that a significantly longer reannealing hybridization was used."

FEATURES
Source

ORIGIN

1. .779
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="NOL00DH3"
/db_xref="taxon:3712"
/clone="BOGXU95"
/clone_id="BOGX"
/note="Vector: phos1; site_1: BstXI; 2-3 kb sheared genomic DNA inserted into phos1 using BstXI linkers."

RESULT 3
CG361559 tigr-GSS-CG361559

LOCUS CG361559 mRNA linear EST 26-AUG-2003
DEFINITION 796 bp DNA clone ZMBMa0739026, genomic survey sequence.

ACCESSION CG361559
VERSION GI:34278826
KEYWORDS
SOURCE Zea mays

ORGANISM *Zea mays*
Eukaryota: Viridiplantae: Streptophytta: Embryophytta: Tracheophytta: Spermatophytta: Magnoliophytta: Liliopsida: Poales: Poaceae: PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Whitehead,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfsing,T., Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.

TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other GSS: OGIDT94TV

TIGR
Contact: Cathy Whitehead
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5543
Fax: 301-838-0208
Email: whitehead@tigr.org
Seq primer: TR

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:59:59 ; Search time 48:42:34 Seconds
(without alignments) 2710.166 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25

Sequence: 1 tcgagaataattgaaataatctatcg 25

Scoring table: Oligo_NUC_60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Word size: 10

Total number of hits satisfying chosen parameters: 72573

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_23Sep04;*

- 1: geneseqn980s;*
- 2: geneseqn990s;*
- 3: geneseqn2000s;*
- 4: geneseqn2001as;*
- 5: geneseqn2001bs;*
- 6: geneseqn2002as;*
- 7: geneseqn2002bs;*
- 8: geneseqn2003as;*
- 9: geneseqn2003bs;*
- 10: geneseqn2003as;*
- 11: geneseqn2003bs;*
- 12: geneseqn2004bs;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	25	100.0	25	5 ARF6138
2	25	100.0	267	5 ARF6166
3	18	72.0	1190	2 ARX13651
4	18	72.0	1190	6 ARB99446
5	18	72.0	5962	6 ARBL3386
6	17	68.0	672	8 ARCA3195
7	17	68.0	177531	8 ARDF62732
8	17	68.0	177531	8 ADB20847
9	17	68.0	177531	10 ADB87936
10	17	68.0	177531	10 ADB96919
11	17	68.0	177531	10 ADB91110
12	17	68.0	177531	10 ADH74517
13	17	68.0	195917	12 ADQ20806
14	16	64.0	358	5 ABV34155
15	16	64.0	64	6 ARN21213
16	16	64.0	455	4 ARB26661
17	16	64.0	497	5 ABV13034
18	16	64.0	1506	10 ACP77932
19	16	64.0	2136	8 AC233650
20	16	64.0	2415	8 ACR43403
21	16	64.0	2426	6 ABQ76758

c	22	16	64.0	3309	4	ABL21530	Drosophil
c	23	16	64.0	6227	2	AAT60141	Antirrhin
c	24	16	64.0	8979	6	ABK32785	Human lmm
c	25	16	64.0	8979	6	ABK3271	Signal tr
c	26	16	64.0	8979	6	ABJ70232	Chemical
c	27	16	64.0	8979	6	AR561179	Human gen
c	28	16	64.0	25426	8	ADA41645	Ada41645 Human sec
c	29	16	64.0	25426	8	ACG50940	Acc50940 Human sec
c	30	16	64.0	25426	10	ADD8135	Add8135 CDNA clon
c	31	16	64.0	25426	10	ADP57777	Ada57777 Bac fragm
c	32	16	64.0	110000	10	ACF67367	Continuation (52 o
c	33	16	64.0	110000	10	ACF65397	Continuation (3 of
c	34	16	64.0	322101	10	ADD58431	Ad58431 Human PRO
c	35	16	64.0	322101	12	ADT35046	Adt35046 Human pro
c	36	15	60.0	656	6	ABN1640	Abn1640 Human ORF
c	37	15	60.0	326	8	ABX5125	Abx5125 Bovine ES
c	38	15	60.0	480	6	ABT10253	Abt10253 Human bre
c	39	15	60.0	525	10	ADD16647	Adi16647 DNA (SeqI
c	40	15	60.0	529	4	AAK56957	Aak56957 Human imm
c	41	15	60.0	529	4	AAI62769	Aai62769 Human cDN
c	42	15	60.0	530	12	ACH71148	Act71148 Human gen
c	43	15	60.0	572	3	AAK87766	Aak87766 Human sec
c	44	15	60.0	572	5	AAE64048	Aae64048 cDNA enco
c	45	15	60.0	572	12	ADP1876	Adp1876 Human sec
c	46	15	60.0	593	5	ABY55376	Abv55376 Human pro
c	47	15	60.0	703	2	AAZ15924	Aaz15924 Human gen
c	48	15	60.0	786	4	AAZ34697	Aah34697 Human col
c	49	15	60.0	854	2	AAZ40809	Aaz40809 Secreted
c	50	15	60.0	854	11	ADM7786	Adm7786 Human sec
c	51	15	60.0	854	12	ADP19107	Adp19107 Human sec
c	52	15	60.0	871	4	AAH03050	Aah03050 Human cDN
c	53	15	60.0	996	8	ACG27493	Acg27493 Prokaryot
c	54	15	60.0	1166	4	AAI16293	Aai16293 Human gen
c	55	15	60.0	1901	4	AAH17036	Aah17036 Human cDN
c	56	15	60.0	2000	6	ABZ15483	Abz15483 Arabidops
c	57	15	60.0	2136	4	AAI62899	Aai62899 Human gen
c	58	15	60.0	2881	10	ADP89810	Adf88810 Tripterpen
c	59	15	60.0	2888	2	AAZ20299	Aaz20299 Berberilla
c	60	15	60.0	3001	3	AAH51775	Aah51775 Chromosome
c	61	15	60.0	3193	4	ABL16198	Abi16198 Drosophill
c	62	15	60.0	3380	4	ABL62151	Abi62151 Drosophill
c	63	15	60.0	3519	8	ACAA3811	Aca3811 Prokaryot
c	64	15	60.0	3552	10	ADC93399	Adc93399 E. facciu
c	65	15	60.0	4338	4	ABL06156	Abi06156 Drosophill
c	66	15	60.0	4785	5	AAST2198	Aas72198 Drosophill
c	67	15	60.0	5064	2	AAV69110	Aav69110 Neisseria
c	68	15	60.0	5276	6	ABJ32151	Abl2151 Human imm
c	69	15	60.0	5276	6	ABJ06156	Abl06156 Drosophill
c	70	15	60.0	5273	4	AAK9320	Aak9320 Pea auxin
c	71	15	60.0	6107	6	ABJ70354	Abl70354 Chemical
c	72	15	60.0	6107	6	ABK61315	Abk61315 Human gen
c	73	15	60.0	6419	15	ABP32267	Abp32267 Human lmm
c	74	15	60.0	6419	15	ABZ52893	Abz52893 Sorghum r
c	75	15	60.0	6760	3	ABJ01880	Abj01880 Drosophill
c	76	15	60.0	7546	4	ABJ334142	Abl334142 Human lmm
c	77	15	60.0	8822	15	ABJ11102	Abl11102 Drosophill
c	78	15	60.0	11021	4	ABJ32906	Abl32906 Drosophill
c	79	15	60.0	1155	15	ABJ3205	Abl3205 Human lmm
c	80	15	60.0	1155	4	ABP09906	Abp09906 Drosophill
c	81	15	60.0	13449	4	ABJ07964	Abj07964 Drosophill
c	82	15	60.0	18624	6	ABJ3703	Abl3703 Human lmm
c	83	15	60.0	22875	4	ABJ28694	Abl28694 Drosophill
c	84	15	60.0	24389	4	ABJ29006	Abl29006 Drosophill
c	85	15	60.0	33472	15	ABJ19792	Abj19792 Human cal
c	86	15	60.0	48000	4	ABP27996	Abp27996 Human cal
c	87	15	60.0	68233	9	ADG66349	Adg66349 Mouse Ppp
c	88	15	60.0	68233	10	ADP10365	Adp10365 Mouse Ppp
c	89	15	60.0	68233	10	ADB2803	Adb2803 Mouse Ppp
c	90	15	60.0	68233	11	ADU27143	Adl27143 Mouse gen
c	91	15	60.0	110000	6	ABR90521	Contamination (16 o
c	92	15	60.0	110000	6	ABR90521	Continuation (20 o
c	93	15	60.0	110000	10	ADU7743	Continuation (10 o
c	94	15	60.0	110000	10	ADL52246	Continuation (2 of

95 15 60.0 112132 6 ABK90888
 95 15 60.0 112132 11 ADM56267
 C 97 15 60.0 121197 5 AAI161370
 98 15 60.0 177851 8 AAL5272 ba438B23-
 C 99 15 60.0 266645 10 Ade87477
 100 15 60.0 340449 8 AAL52198

ALIGNMENTS

RESULT 1 abk90888 Human ATP
 AAf61638 standard; DNA; 25 BP.
 ID AAF61638 standard; DNA; 267 BP.
 XX
 AC AAF61638;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Lactobacillus brevis 23S rRNA/5S rRNA specific probe SEQ ID 73.
 XX
 KW 23S rRNA; detection; probe; brewing; beer; contamination; ss.
 XX
 OS Lactobacillus brevis.
 XX
 PN DE19945964-A1.
 XX
 PD 05-APR-2001.
 XX
 PR 24-SEP-1999; 99DE-01045964.
 XX
 PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 PI Pandke M, Gasch A, Berghof K;
 PR DE19945964-A1.
 XX
 DR WPI; 2001-246136/26.
 XX
 PT Detecting contaminating microorganisms in brewing, by nucleic acid
 amplification and hybridization, either non-specific or genus- or species
 -specific.
 XX
 PS Claim 9(i); Page 9; 48PP; German.

RESULT 2 abk90888 Human ATP
 AAf61566 standard; DNA; 267 BP.
 ID AAF61566 standard; DNA; 267 BP.
 XX
 AC AAF61566;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.
 XX
 KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
 XX
 OS Lactobacillus brevis.
 XX
 PN DE19945964-A1.
 XX
 PD 05-APR-2001.
 XX
 PR 24-SEP-1999; 99DE-01045964.
 XX
 PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 PI Pandke M, Gasch A, Berghof K;
 PR DE19945964-A1.
 XX
 DR WPI; 2001-246136/26.

RESULT 1 abk90888 Human ATP
 AAf61638 standard; DNA; 25 BP.
 ID AAF61638 standard; DNA; 267 BP.
 XX
 AC AAF61638;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Lactobacillus brevis 23S rRNA/5S rRNA specific probe SEQ ID 73.
 XX
 KW 23S rRNA; detection; probe; brewing; beer; contamination; ss.
 XX
 OS Lactobacillus brevis.
 XX
 PN DE19945964-A1.
 XX
 PD 05-APR-2001.
 XX
 PR 24-SEP-1999; 99DE-01045964.
 XX
 PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
 PI Pandke M, Gasch A, Berghof K;
 PR DE19945964-A1.
 XX
 DR WPI; 2001-246136/26.

This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub)species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

XX
 Sequence 25 BP; 11 A; 2 C; 4 G; 8 T; 0 U; 0 Other;
 SQ 100.0%; Score 25; DB 5; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.0015; Mismatches 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCGAGATTAATGATAATATCTAG 25
 Db 125 TCGAGATTAATGATAATATCTAG 149
 XX
 RESULT 3 AAX13651/c
 ID AAX13651 standard; DNA; 1190 BP.
 XX
 AC AAX13651;
 XX
 DT 19-MAR-1999 (first entry)
 XX
 DE Enterococcus faecalis genome contig SEQ ID NO:714.
 XX
 KW Enterococcus faecalis; contig; detection; Enterococcal infection;

Query Match Best Local Similarity 100.0%; Pred. No. 0.0015; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TCGAGATTAATGATAATATCTAG 25
 Db 1 TCGAGATTAATGATAATATCTAG 25

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Om nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:28:49 ; Search time 36.1351. Seconds
 (without alignments)
 3138.794 Million cell updates/sec

Title: US-10-088-666-21
 Perfect score: 21
 Sequence: 1 cccatgttcaacaacgttttgt 21

Scoring table: Oligo_NUC ;
 Gapop 60.0 , Gapext 60.0

Searched: 3625171 seqs, 2700493622 residues

Word size : 10^7

Total number of hits satisfying chosen parameters: 28758

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Published Applications NA:*

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 2: /cgmn_6/prodata/2/pubpna/pctc_NEW_PUB.seq: *
 3: /cgmn_6/prodata/2/pubpna/us06_NEW_PUB.seq: *
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 5: /cgmn_6/prodata/2/pubpna/us07_NEW_PUB.seq: *
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 12: /cgmn_6/prodata/2/pubpna/us08_NEW_PUB.seq: *
 13: /cgmn_6/prodata/2/pubpna/us09_PUBCOMB.seq: *
 14: /cgmn_6/prodata/2/pubpna/us09_PUBCOMB.seq: *
 15: /cgmn_6/prodata/2/pubpna/us10c_PUBCOMB.seq: *
 16: /cgmn_6/prodata/2/pubpna/us10c_PUBCOMB.seq: *
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 18: /cgmn_6/prodata/2/pubpna/us10c_PUBCOMB.seq: *
 19: /cgmn_6/prodata/2/pubpna/us11c_PUBCOMB.seq: *
 20: /cgmn_6/prodata/2/pubpna/us11c_PUBCOMB.seq: *
 21: /cgmn_6/prodata/2/pubpna/us60c_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	16	76.2	365 16 US-10-424-599-100843	Sequence 100843, Sequence 97644, A
c	15	71.4	395 16 US-10-424-599-97864	Sequence 4222, AP Sequence 3096, A
c	15	71.4	621 17 US-10-767-95-222	Sequence 3096, A
c	15	71.4	741 15 US-10-369-493-30596	Sequence 20775, A
c	15	71.4	1134 16 US-10-425-115-20775	Sequence 16778, A
c	15	71.4	1156 16 US-10-425-115-16878	Sequence 10548, A
c	15	71.4	1161 16 US-10-424-99-10548	Sequence 49881, A
c	15	71.4	1188 16 US-10-424-599-97861	Sequence 133586, A
c	15	71.4	16876 13 US-10-437-963-8813	Sequence 1421, APP Sequence 8513, AP
c	14	66.7	254 17 US-10-027-632-241832	Sequence 241832, A
c	13	55.9	US-10-027-632-241832	Sequence 241832, A
c	14	66.7	561 15 US-10-437-963-32347	Sequence 7736, AP
c	15	66.7	591 15 US-10-039-386-7735	Sequence 199748, AP
c	16	66.7	601 13 US-10-037-632-199748	Sequence 199749, AP
c	17	66.7	601 13 US-10-037-632-199748	Sequence 199749, AP
c	18	66.7	601 15 US-10-037-632-199749	Sequence 199749, AP
c	19	66.7	601 15 US-10-037-632-199749	Sequence 199749, AP
c	20	66.7	1203 13 US-10-037-632-199747	Sequence 199747, AP
c	21	66.7	1203 15 US-10-037-632-199747	Sequence 199747, AP
c	22	66.7	1613 17 US-10-451-467A-259	Sequence 259, AP
c	23	66.7	1650 16 US-10-282-122A-31915	Sequence 199745, AP
c	24	66.7	1820 17 US-10-317-963-97628	Sequence 97628, AP
c	25	66.7	2000 16 US-10-200-238-1774	Sequence 1734, AP
c	26	66.7	2347 16 US-10-424-593-54100	Sequence 54300, AP
c	27	66.7	2732 15 US-10-369-493-36202	Sequence 36202, AP
c	28	66.7	2796 17 US-10-437-963-97626	Sequence 97626, AP
c	29	66.7	3825 9 US-09-740-491-11	Sequence 11, APP
c	30	66.7	19639 8 US-08-910-3865-6	Sequence 6, APP
c	31	66.7	147939 13 US-10-087-192-442	Sequence 442, APP
c	32	61.9	147939 15 US-10-038-263B-47779	Sequence 47079, AP
c	33	61.9	180 17 US-10-737-701-23303	Sequence 23203, AP
c	34	61.9	207 9 US-09-960-352-4229	Sequence 4229, AP
c	35	61.9	211 9 US-09-960-352-2061	Sequence 2061, AP
c	36	61.9	229 9 US-09-960-352-4220	Sequence 4220, AP
c	37	61.9	239 9 US-09-960-352-13451	Sequence 13451, AP
c	38	61.9	242 9 US-09-960-352-2998	Sequence 2998, AP
c	39	61.9	247 9 US-09-960-352-183	Sequence 183, APP
c	40	61.9	281 9 US-09-960-352-9850	Sequence 9850, AP
c	41	61.9	292 9 US-09-960-352-7737	Sequence 7737, AP
c	42	61.9	301 9 US-09-960-352-1032	Sequence 10392, AP
c	43	61.9	313 9 US-09-960-352-2061	Sequence 104720, AP
c	44	61.9	310 16 US-10-424-599-107220	Sequence 692, APP
c	45	61.9	324 10 US-09-74-891-692	Sequence 3253, A
c	46	61.9	324 10 US-10-031-572-56	Sequence 3253, A
c	47	61.9	325 17 US-10-437-963-31353	Sequence 6697, AP
c	48	61.9	325 17 US-10-437-963-31353	Sequence 6698, AP
c	49	61.9	337 10 US-09-764-891-6697	Sequence 558, APP
c	50	61.9	337 14 US-10-031-572-558	Sequence 559, APP
c	51	61.9	337 14 US-10-031-572-559	Sequence 2661, AP
c	52	61.9	340 9 US-09-960-352-2761	Sequence 2191, AP
c	53	61.9	341 9 US-09-960-352-2191	Sequence 2191, AP
c	54	61.9	341 16 US-10-424-599-12828	Sequence 114828, A
c	55	61.9	342 9 US-09-960-352-11482	Sequence 9403, AP
c	56	61.9	343 13 US-09-960-352-11482	Sequence 8472, AP
c	57	61.9	348 9 US-09-960-352-9403	Sequence 2079, AP
c	58	61.9	350 9 US-09-960-352-597	Sequence 12857, A
c	59	61.9	356 9 US-09-960-352-12837	Sequence 8659, AP
c	60	61.9	356 9 US-09-960-352-12837	Sequence 14094, A
c	61	61.9	366 9 US-09-960-352-14094	Sequence 4223, AP
c	62	61.9	368 13 US-09-960-352-4223	Sequence 2966, AP
c	63	61.9	378 9 US-09-960-352-2961	Sequence 215, APP
c	64	61.9	382 9 US-09-960-352-215	Sequence 30666, A
c	65	61.9	384 9 US-10-677-701-30666	Sequence 10641, A
c	66	61.9	385 9 US-09-960-352-10641	Sequence 13175, A
c	67	61.9	387 9 US-09-960-352-1175	Sequence 9798, AP
c	68	61.9	391 9 US-09-960-352-10595	Sequence 2505, AP
c	69	61.9	395 9 US-09-960-352-2505	Sequence 7013, AP
c	70	61.9	398 9 US-09-960-352-7013	Sequence 9396, AP
c	71	61.9	399 9 US-09-960-352-9396	Sequence 179, APP
c	72	61.9	404 9 US-09-960-352-179	Sequence 2795, AP
c	73	61.9	404 9 US-09-960-352-9889	Sequence 9889, AP
c	74	61.9	404 9 US-09-960-352-9795	Sequence 7246, AP
c	75	61.9	404 9 US-09-960-352-9795	Sequence 7246, AP
c	76	61.9	405 9 US-09-960-352-7246	Sequence 766, AP
c	77	61.9	405 10 US-09-960-352-45529	Sequence 45529, AP
c	78	61.9	405 10 US-09-960-352-12380	Sequence 12380, A
c	79	61.9	406 9 US-09-960-352-9845	Sequence 9845, AP
c	80	61.9	407 9 US-09-960-352-11517	Sequence 11517, AP
c	81	61.9	416 9 US-09-960-352-11517	Sequence 10053, A
c	82	61.9	417 9 US-09-960-352-10053	Sequence 124751, AP
c	83	61.9	417 15 US-09-960-352-12751	Sequence 7509, AP
c	84	61.9	419 9 US-09-960-352-7509	Sequence 6117, AP
c	85	61.9	420 9 US-09-960-352-6117	Sequence 241832, A

୨୮

RESULT 1
US-10-424-599-100843
; Sequence 100843, Application US/10424599
; Publication No. US20040031072A1

GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21-(5323)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 100843
; LENGTH: 365
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_62074C.1
US-10-424-599-100843

Query Match 76.2%; Score 16; DB 16; Length 365;
Best Local Similarity 100.0%; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
Matches 16; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 4 AGTCACAACTAGT 19
Db 124 AGTCACAACTAGT 139

RESULT 2
US-10-424-599-97864/c
; Sequence 97864, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21-(5323)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 97864
; LENGTH: 395
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_59395C.1
US-10-424-599-97864

Query Match 71.4%; Score 15; DB 15; Length 395;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCACAACTAGT 15
Db 88 CCAGTCACAACTAGT 102

ALIGNMENTS

RESULT 3
US-10-767-795-4222/c
; Sequence 4222, Application US/10767795
; Publication No. US20040181830A1

GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Zhou, Yihua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21-(5353)B
; CURRENT APPLICATION NUMBER: US/10/767,795
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 117596
; SEQ ID NO 4222
; LENGTH: 621
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: GOSHI-09MAY01-CU11_9
US-10-767-795-4222

Query Match 71.4%; Score 15; DB 17; Length 621;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 3 AGTCACAACTAGT 17
Db 87 AGTCACAACTAGT 73

RESULT 4
US-10-369-493-30596
; Sequence 30596, Application US/10369493
; Publication No. US20030233675A1

GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldham, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10-(5202)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIORITY FILING DATE: 2002-07-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 30596
; LENGTH: 741
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-369-493-30596

Query Match 71.4%; Score 15; DB 15; Length 741;
Best Local Similarity 100.0%; Pred. No. 40; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCACAACTAGT 15
Db 88 CCAGTCACAACTAGT 102

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 14:18:54 ; Search time 8.95496 Seconds
(without alignments)
1666.850 Million cell updates/sec

Title: US-10-088-666-21
Perfect score: 21
Sequence: 1 ccaagtaaacaaatggatgtt 21

Scoring table: Oligo-NUC,
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 35539441 residues

Wordsize: 10

Total number of hits satisfying chosen parameters: 4843

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:
 1: /cggn_6/podata/1/ina/5A_COMB.seq: *
 2: /cggn_6/podata/1/ina/5B_COMB.seq: *
 3: /cggn_6/podata/1/ina/6A_COMB.seq: *
 4: /cggn_6/podata/1/ina/6B_COMB.seq: *
 5: /cggn_6/podata/1/ina/PCTUS_COMB.seq: *
 6: /cggn_6/podata/1/ina/backfiles.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	14	66.7	610 4	US-09-270-767-12339 Sequence 12339, AP
2	13	61.9	186 4	US-09-248-796A-4468 Sequence 7468, AP
3	13	61.9	189 4	US-09-583-110-2297 Sequence 2597, AP
4	13	61.9	360 4	US-09-134-000C-796 Sequence 2796, AP
5	13	61.9	396 4	US-09-252-991A-6239 Sequence 6239, AP
6	13	61.9	525 4	US-09-248-796A-1527 Sequence 1527, AP
7	13	61.9	564 4	US-09-250-2598 Sequence 2598, AP
8	13	61.9	639 4	US-09-248-796A-6795 Sequence 6195, AP
9	13	61.9	708 1	US-07-794-398B-1 Sequence 1, APPLI
10	13	61.9	708 1	US-08-002-886-1 Sequence 1, APPLI
11	13	61.9	780 4	US-09-248-796A-4461 Sequence 6461, AP
12	13	61.9	954 4	US-09-248-796A-3947 Sequence 2947, AP
13	13	61.9	963 4	US-09-328-762-3811 Sequence 3811, AP
14	13	61.9	997 4	US-09-690-454-33 Sequence 33, APPLI
15	13	61.9	1089 4	US-09-291-194-3 Sequence 5, APPLI
16	13	61.9	1101 4	US-09-248-796A-1389 Sequence 1389, AP
17	13	61.9	1236 4	US-09-016-434-717 Sequence 717, AP
18	13	61.9	1243 1	US-08-702-34-27 Sequence 27, APPLI
19	13	61.9	1266 4	US-09-248-796A-314 Sequence 314, AP
20	13	61.9	1272 4	US-09-489-039A-5398 Sequence 5398, AP
21	13	61.9	1295 4	US-09-219-194-3 Sequence 3, APPLI
22	13	61.9	1299 4	US-09-248-796A-5857 Sequence 5857, AP
23	13	61.9	1302 4	US-09-270-767-15521 Sequence 1021, AP
24	13	61.9	1311 4	US-09-248-796A-5537 Sequence 5537, AP
25	13	61.9	1317 4	US-09-248-796A-5750 Sequence 5750, AP
26	13	61.9	1318 4	US-09-270-767-2088 Sequence 2908, AP
27	13	61.9	1356 4	US-09-489-039A-5355 Sequence 5355, AP

c 28 13 61.9 1413 4 US-09-134-000C-2063 Sequence 2063, AP
c 30 13 61.9 1505 4 US-09-291-299A-2 Sequence 2, APPLI
c 31 13 61.9 1950 4 US-09-270-767-13177 Sequence 13177, A
c 32 13 61.9 2073 4 US-09-241-796A-50566 Sequence 50566, AP
c 33 13 61.9 2130 4 US-09-583-110-2452 Sequence 2452, AP
c 34 13 61.9 2133 4 US-09-248-796A-302 Sequence 302, APPLI
c 35 13 61.9 2218 2 US-08-421-044-1 Sequence 1, APPLI
c 36 13 61.9 2307 4 US-09-791-024-43 Sequence 43, APPLI
c 37 13 61.9 2542 1 US-08-411-370-1 Sequence 1, APPLI
c 38 13 61.9 2669 1 US-08-118-101A-3 Sequence 3, APPLI
c 39 13 61.9 2670 4 US-09-614-221A-540 Sequence 540, APPLI
c 40 13 61.9 4565 3 US-08-776-265-2 Sequence 2, APPLI
c 41 13 61.9 4565 4 US-09-398-184-2 Sequence 2, APPLI
c 42 13 61.9 5240 3 US-09-171-331A-2 Sequence 2, APPLI
c 43 13 61.9 5240 4 US-09-631-222-2 Sequence 2, APPLI
c 44 13 61.9 8791 5 PCT-US96-0175-5 Sequence 5, APPLI
c 45 13 61.9 9610 4 US-09-566-921-45 Sequence 45, APPLI
c 46 13 61.9 9840 4 US-09-385-222A-3 Sequence 3, APPLI
c 47 13 61.9 15363 4 US-08-961-527-139 Sequence 139, APPLI
c 48 12 57.1 28 1 US-07-720-513-9 Sequence 9, APPLI
c 49 12 57.1 85 1 US-08-961-527-139 Sequence 9, APPLI
c 50 12 57.1 90 3 US-08-974-549A-685 Sequence 685, APPLI
c 51 12 57.1 90 4 US-08-974-549A-686 Sequence 685, APPLI
c 52 12 57.1 90 4 US-09-721-456-686 Sequence 685, APPLI
c 53 12 57.1 90 4 US-09-721-456-686 Sequence 685, APPLI
c 54 12 57.1 108 5 PCT-US95-09589-6 Sequence 6, APPLI
c 55 12 57.1 108 5 PCT-US95-09589-A-6 Sequence 6, APPLI
c 56 12 57.1 237 4 US-09-513-999C-30318 Sequence 605, APPLI
c 57 12 57.1 257 4 US-09-252-991A-6214 Sequence 6214, APPLI
c 58 12 57.1 286 4 US-09-270-767-14783 Sequence 14783, APPLI
c 59 12 57.1 291 4 US-09-313-294A-6338 Sequence 6338, APPLI
c 60 12 57.1 324 4 US-09-721-456-686 Sequence 10980, APPLI
c 61 12 57.1 330 5 PCT-US95-09589-1 Sequence 1, APPLI
c 62 12 57.1 330 5 PCT-US95-09589A-1 Sequence 1, APPLI
c 63 12 57.1 350 2 US-08-967-101-35 Sequence 35, APPLI
c 64 12 57.1 350 2 US-08-592-541-35 Sequence 35, APPLI
c 65 12 57.1 350 3 US-09-124-698-35 Sequence 35, APPLI
c 66 12 57.1 350 3 US-08-490-841C-35 Sequence 35, APPLI
c 67 12 57.1 350 3 US-09-124-523-35 Sequence 35, APPLI
c 68 12 57.1 350 4 US-08-636-798A-35 Sequence 35, APPLI
c 69 12 57.1 350 4 US-08-431-04F-35 Sequence 35, APPLI
c 70 12 57.1 350 4 US-08-016-434-707 Sequence 707, APPLI
c 71 12 57.1 368 4 US-09-114-000C-1089 Sequence 1089, APPLI
c 72 12 57.1 372 4 US-09-056-434-707 Sequence 1089, APPLI
c 73 12 57.1 400 4 US-08-956-171E-374 Sequence 3674, APPLI
c 74 12 57.1 400 4 US-08-781-986S-3674 Sequence 3674, APPLI
c 75 12 57.1 432 4 US-09-248-796S-3994 Sequence 3904, APPLI
c 76 12 57.1 444 4 US-09-248-796A-8888 Sequence 8288, APPLI
c 77 12 57.1 454 4 US-09-221-017B-179 Sequence 179, APPLI
c 78 12 57.1 457 4 US-09-210-767-1019 Sequence 10199, APPLI
c 79 12 57.1 461 4 US-09-513-999C-4086 Sequence 4086, APPLI
c 80 12 57.1 462 4 US-09-270-767-10077 Sequence 10077, APPLI
c 81 12 57.1 551 4 US-09-248-796S-32 Sequence 32, APPLI
c 82 12 57.1 555 4 US-09-270-767-26085 Sequence 26085, APPLI
c 83 12 57.1 564 4 US-09-593-681A-2875 Sequence 2575, APPLI
c 84 12 57.1 570 3 US-08-988-416-159 Sequence 159, APPLI
c 85 12 57.1 600 4 US-09-335-932A-6 Sequence 6, APPLI
c 86 12 57.1 615 4 US-09-956-171E-3638 Sequence 5223, APPLI
c 87 12 57.1 618 4 US-09-543-681A-3028 Sequence 3028, APPLI
c 88 12 57.1 624 3 US-09-415-522-1 Sequence 1, APPLI
c 89 12 57.1 624 3 US-09-593-681A-12 Sequence 12, APPLI
c 90 12 57.1 645 4 US-09-252-991A-6331 Sequence 6331, APPLI
c 91 12 57.1 668 4 US-08-956-171E-3638 Sequence 3658, APPLI
c 92 12 57.1 668 4 US-09-488-796S-523 Sequence 5223, APPLI
c 93 12 57.1 735 4 US-09-328-352-1471 Sequence 1471, APPLI
c 94 12 57.1 749 4 US-09-210-767-13258 Sequence 13258, APPLI
c 95 12 57.1 778 4 US-09-355-932A-7 Sequence 7, APPLI
c 96 12 57.1 783 4 US-09-592-991A-6415 Sequence 6415, APPLI
c 97 12 57.1 819 3 US-08-441-857-3 Sequence 3, APPLI
c 98 12 57.1 819 3 US-08-422-807A-31 Sequence 3, APPLI
c 99 12 57.1 819 3 US-09-252-991A-6136 Sequence 6136, APPLI

ALIGNMENTS

RESULT 1 ; CURRENT FILING DATE: 2000-05-26
 US-09-270-767-12339 ; PRIOR APPLICATION NUMBER: US 09/107,433
 ; Sequence 12339, Application US/09270767
 ; PATENT NO. 6703491 ; PRIOR FILING DATE: 1998-06-30
 ; APPLICANT: Homburger et al. ; PRIOR APPLICATION NUMBER: US 60/085,131
 ; GENERAL INFORMATION: ; PRIOR FILING DATE: 1998-05-12
 ; TITLE OF INVENTION: Nucleic acids and Proteins of *Drosophila melanogaster* ; PRIOR APPLICATION NUMBER: US 60/051,553
 ; FILE REFERENCE: File Reference: 7326-094 ; PRIOR FILING DATE: 1997-07-02
 ; CURRENT APPLICATION NUMBER: US/09/270,767 ; NUMBER OF SEQ ID NOS: 5322
 ; CURRENT FILING DATE: 1999-03-17 ; SEQ ID NO 2597
 ; NUMBER OF SEQ ID NOS: 62517 ; LENGTH: 189
 ; SOFTWARE: PatentIn Ver. 2.0 ; TYPE: DNA
 ; SEQ ID NO 12339 ; ORGANISM: *Streptococcus pneumoniae*
 ; LENGTH: 610 ; US-09-583-110-2597
 ; TYPE: DNA ; ORGANISM: *Drosophila melanogaster*
 ; US-09-270-767-12339 ;
 ;
 Query Match 56.7%; Score 14; DB 4; Length 610;
 Best Local Similarity 100.0%; Pred. No. 16; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GTGACAACTAGT 18 ;
 Db 498 GTCAACAACTAGT 511 ;
 ;
 RESULT 2 ;
 US-09-248-796A-7468 ;
 ; Sequence 7468, Application US/09248796A ;
 ; Patient No. 6747137 ;
 ; GENERAL INFORMATION: ;
 ; APPLICANT: Keith Weinstock et al ;
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS ;
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN ;
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS ;
 ; FILE REFERENCE: 107196-132 ;
 ; CURRENT APPLICATION NUMBER: US/09/248,796A ;
 ; PRIOR FILING DATE: 1999-02-12 ;
 ; CURRENT FILING DATE: 1998-02-13 ;
 ; PRIOR FILING DATE: 1998-08-13 ;
 ; NUMBER OF SEQ ID NOS: 28208 ;
 ; SEQ ID NO 7468 ;
 ; LENGTH: 186 ;
 ; TYPE: DNA ;
 ; ORGANISM: *Candida albicans*
 ; US-09-248-796A-7468 ;
 ;
 Query Match 61.9%; Score 13; DB 4; Length 186;
 Best Local Similarity 100.0%; Pred. No. 61; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGAGTCACAC 13 ;
 Db 4 CCGAGTCACAC 16 ;
 ;
 RESULT 3 ;
 US-09-583-110-2597/c ;
 ; Sequence 2597, Application US/09583110 ;
 ; Patient No. 6699703 ;
 ; GENERAL INFORMATION: ;
 ; APPLICANT: Lynn Doucette-Stamm et al. ;
 ; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus ;
 ; FILE REFERENCE: PATH00-07A ;
 ; CURRENT APPLICATION NUMBER: US/09/583,110 ;
 ;
 Query Match 61.9%; Score 13; DB 4; Length 360;
 Best Local Similarity 100.0%; Pred. No. 62; Mismatches 0; Indels 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCAAGTCAACAC 13 ;
 Db 265 CCAAGTCAACAC 253 ;
 ;
 RESULT 5 ;
 US-09-252-991A-6239 ;
 ; Sequence 6239, Application US/09252991A ;
 ; Patient No. 6551195 ;
 ; GENERAL INFORMATION: ;
 ; APPLICANT: Marc J. Rubenfeld et al. ;
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ;
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ;
 ; FILE REFERENCE: 107195-136 ;
 ; CURRENT APPLICATION NUMBER: US/09/252,991A ;
 ; CURRENT FILING DATE: 1999-02-18 ;
 ; PRIOR APPLICATION NUMBER: US 60/074,788 ;
 ; PRIOR FILING DATE: 1998-02-18 ;
 ; PRIOR APPLICATION NUMBER: US 60/094,190 ;
 ; PRIOR FILING DATE: 1998-07-27 ;
 ; NUMBER OF SEQ ID NOS: 33142 ;
 ; SEQ ID NO 6239 ;
 ; LENGTH: 396 ;
 ; TYPE: DNA ;
 ; ORGANISM: *Pseudomonas aeruginosa*

Run on: November 15, 2004, 11:59:59 ; Search time 40,6757 seconds
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OM nucleic - nucleic search, using sw model

Title: US-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagtcaacaaacgttgtt 21

Scoring table: Oligo_NUC

Gappen 60.0 , Gapext 60.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 31333

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : N_Geneseq_21sep04:*

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2: geneseqn2000s;*

3: geneseqn201as;*

4: geneseqn201bs;*

5: geneseqn2002as;*

6: geneseqn2002bs;*

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8: geneseqn2003bs;*

9: geneseqn2003as;*

10: geneseqn2003bs;*

11: geneseqn2003ds;*

12: geneseqn2004s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	21	5 AAF61586
2	21	100.0	21	5 AAF61586 Lactobaci
3	18	85.7	2215	3 AAZ43884 C. vicina
4	14	66.7	546	6 ABN2311 Human ORF
5	14	66.7	591	12 ACH4541
6	14	66.7	668	3 AAF13909 Aspergillus
7	14	66.7	729	6 ABS62906 Selected
8	14	66.7	729	6 ABT1511 Yeast sel
9	14	66.7	750	11 ADM4774 Insect re
10	14	66.7	766	6 ABS62991
11	14	66.7	766	6 ABT1596 Yeast sel
12	14	66.7	789	10 ADK4602 Plant DNA
13	14	66.7	789	11 ADM45503 Insect re
14	14	66.7	812	6 ABS63068 Selected
15	14	66.7	813	6 ABT11673 Yeast sel
16	14	66.7	935	10 ADC72643 DNA Seq I
17	14	66.7	935	10 ADC72635 DNA Seq I
18	14	66.7	1613	6 ABQ7617 S. cerevi
19	14	66.7	1650	8 ACA4345 Prokaryot
20	14	66.7	1680	4 ADL21577 Drosophil
21	14	66.7	2000	12 ADJ40734 Plant cDN

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	21	5 AAF61586
2	21	100.0	21	5 AAF61586 Lactobaci
3	18	85.7	2215	3 AAZ43884 C. vicina
4	14	66.7	546	6 ABN2311 Human ORF
5	14	66.7	591	12 ACH4541
6	14	66.7	668	3 AAF13909 Aspergillus
7	14	66.7	729	6 ABS62906 Selected
8	14	66.7	729	6 ABT1511 Yeast sel
9	14	66.7	750	11 ADM4774 Insect re
10	14	66.7	766	6 ABS62991
11	14	66.7	766	6 ABT1596 Yeast sel
12	14	66.7	789	10 ADK4602 Plant DNA
13	14	66.7	789	11 ADM45503 Insect re
14	14	66.7	812	6 ABS63068 Selected
15	14	66.7	813	6 ABT11673 Yeast sel
16	14	66.7	935	10 ADC72643 DNA Seq I
17	14	66.7	935	10 ADC72635 DNA Seq I
18	14	66.7	1613	6 ABQ7617 S. cerevi
19	14	66.7	1650	8 ACA4345 Prokaryot
20	14	66.7	1680	4 ADL21577 Drosophil
21	14	66.7	2000	12 ADJ40734 Plant cDN

Add7799	Human	gen
Adn3951	Human	pro
Aac86158	PCTR6	nuc
AbI21576	Drosophil	
Aax23524	O.	longis
Continuation	(11	o
Act147088	Human	mic
Aab71387	Streptoco	
Adk33539	Polyrucle	
Abx33064	Bovine	ES
Abx6896	Bovine	ES
Abx35050	Bovine	ES
Abx6286	Bovine	ES
Abx33833	Bovine	ES
Absc6927	Selected	
Abt11532	Yeast	sel
Aba35198	Bovine	ES
Aai69393	Prokrae	m19
Abx44685	Bovine	ES
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Abx34921	Bovine	ES
Abx45227	Bovine	ES
Aal10691	Human	rep
Aas40105	DNA	encod
Aab33756	Bovine	ES
Abx7026	Bovine	ES
Abx45317	Bovine	ES
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Abx4238	Bovine	ES
Ath30860	Human	col
Abx33077	Bovine	ES
Aak38556	Human	sec
Abx6914	Bovine	ES
Aab47692	Bovine	ES
Abr2911	Enterococ	
Adm19610	Novel	hum
Aabx3494	Bovine	ES
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Abx37801	Bovine	ES
Abx3050	Bovine	ES
Abx5476	Bovine	ES
Abx8010	Bovine	ES
Abx5430	Bovine	ES
Abx37340	Bovine	ES
Aabx76735	Pseudomon	
Aak2170	Human	lmm
Abx1848	Bovine	ES
Abr4421	Bovine	ES
Abx44724	Bovine	ES
Abx35014	Bovine	ES
Abr37630	Bovine	ES
Aac1811	Arabidops	
Aabx4352	Bovine	ES
Abx4344	Bovine	ES
Abx2081	Bovine	ES
Abx47215	Bovine	ES
Abrx4681	Bovine	ES
Aac1759	Arabidops	
Abrx6352	Bovine	ES
Abx4344	Bovine	ES
Abrx1052	Bovine	ES
Abx2638	Bovine	ES
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95 13 61.9 444 6 ABN68526
 96 13 61.9 455 9 ACU17009
 Abz2858 Aspergillus
 97 13 61.9 456 8 ABX43980
 Abx3398 Bovine ES
 98 13 61.9 458 8 ADG3705
 Add37805 Aspergill
 99 13 61.9 489 10 Aai33114 Probe #18
 c 100 13 61.9 499 4 Aai33114

ALIGNMENTS

RESULT 1
 ID AAF61586
 XX AAF61586 standard; DNA; 21 BP.
 AC AAF61586;
 XX DT 02-JUL-2001 (first entry)
 XX DE Lactobacillus brevis 23S rRNA/5S rRNA specific DNA probe.
 XX KW 23S rRNA; detection; probe; brewing; beer; contamination; ss.
 OS Lactobacillus brevis.
 XX PR DE19945964-A1.
 XX PN 05-APR-2001.
 XX PF 24-SEP-1999; 99DE-01045964.
 XX PR 24-SEP-1999; 99DE-01045964.
 XX PA (BIOT-) BIOTCON DIAGNOSTICS GMBH.
 XX PI Fandke M., Gasch A., Bergnaf K.;
 PN DR WPI; 2001-246136/26.
 XX PT Detecting contaminating microorganisms in brewing by nucleic acid amplification and hybridization, either non-specific or genus- or species -specific.
 XX PT Claim 9(i); Page 9; 48pp; German.
 XX PS This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub)species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

Abn68526 Streptococcus
 AcU17009 DNA clone
 Abz2858 Aspergillus
 Abx3398 Bovine ES
 Add37805 Aspergillus
 Aai33114 Probe #18

RESULT 2
 ID AAF61566
 XX AAF61566 standard; DNA; 267 BP.
 AC AAF61566;
 XX DT 02-JUL-2001 (first entry)

XX DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.
 XX KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
 OS Lactobacillus brevis.

RESULT 1
 ID AAF61586
 XX AAF61586 standard; DNA; 21 BP.
 AC AAF61586;
 XX DT 02-JUL-2001 (first entry)
 XX DE Lactobacillus brevis 23S rRNA/5S rRNA specific DNA probe.
 XX KW 23S rRNA; detection; probe; brewing; beer; contamination; ss.
 OS Lactobacillus brevis.

XX PR DE19945964-A1.
 XX PN 05-APR-2001.
 XX PF 24-SEP-1999; 99DE-01045964.
 XX PR 24-SEP-1999; 99DE-01045964.
 XX PA (BIOT-) BIOTCON DIAGNOSTICS GMBH.
 XX PI Fandke M., Gasch A., Bergnaf K.;
 PN DR WPI; 2001-246136/26.

XX PT Detecting contaminating microorganisms in brewing by nucleic acid amplification and hybridization, either non-specific or genus- or species -specific.

XX PT Claim 9(i); Page 9; 48pp; German.

XX PS This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub)species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

XX SQ Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;
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XX DT 10-MAR-2000 (first entry)

XX DE C. vicina LSP-2 cDNA.
 XX KW Arylporin; calliphorin; ABP; receptor-binding domain; plant protection;

RESULT 3
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 AC AAZ43884;
 XX DT 10-MAR-2000 (first entry)

XX DE C. vicina LSP-2 cDNA.
 XX KW Arylporin; calliphorin; ABP; receptor-binding domain; plant protection;

RESULT 1
 ID AAF61586
 XX AAF61586 standard; DNA; 21 BP.
 AC AAF61586;
 XX DT 02-JUL-2001 (first entry)
 XX DE Lactobacillus brevis 23S rRNA/5S rRNA specific DNA probe.
 XX KW 23S rRNA; detection; probe; brewing; beer; contamination; ss.
 OS Lactobacillus brevis.

XX PR DE19945964-A1.
 XX PN 05-APR-2001.
 XX PF 24-SEP-1999; 99DE-01045964.
 XX PR 24-SEP-1999; 99DE-01045964.
 XX PA (BIOT-) BIOTCON DIAGNOSTICS GMBH.
 XX PI Fandke M., Gasch A., Bergnaf K.;
 PN DR WPI; 2001-246136/26.

XX PT Detecting contaminating microorganisms in brewing by nucleic acid amplification and hybridization, either non-specific or genus- or species -specific.

XX PT Claim 9(i); Page 9; 48pp; German.

XX PS This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub)species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis

XX SQ Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;
 Query Match 100.0%; Score 21; DB 5; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0.024; Mismatches 0; Indels 0; Gaps 0;

XX DT 10-MAR-2000 (first entry)

Query Match 100.0%; Score 21; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCACAACTAGTGT 21
 Db 1 CCAAGTCACAACTAGTGT 21

XX DE C. vicina LSP-2 cDNA.

XX KW Arylporin; calliphorin; ABP; receptor-binding domain; plant protection;

Run on: OM nucleic - nucleic search, using SW model
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November 15, 2004, 12:43:29 ; Search time 163.964 seconds
(without alignments)
6056.719 Million cell updates/sec

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Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 181462

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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11: gb_sts: *
12: gb_sy: *
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14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
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8	16	76.2	40639	2	ACI29903	ACI29903 Ciona sav
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11	16	76.2	11000	8	CRS80949	CRS80949 Continuation (4 of
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14	16	76.2	17024	2	ACI146726	ACI146726 Otolomus
15	16	76.2	19857	2	ACI116847	ACI116847 Mus musculus
16	16	76.2	228453	2	ACI46729	ACI46729 Octolemus
17	16	76.2	254684	2	AC094805	AC094805 Rattus no
18	16	76.2	261162	1	AB017257	AB017257 Wolbachia
19	16	76.2	268619	2	ACI30037	ACI30037 Rattus no

RESULT 1
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 ACCESSION AX105749
 VERSION AX105749.1 GI:13921762
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM artificial sequences.
 REFERENCE 1.
 AUTHORS Fandke,M., Gusch,A. and Berghof,K.
 TITLE Method and nucleic acids for determining the presence of
 micro-organisms specific to the brewing process
 JOURNAL Patent: WO 0123605-A 21 05-APR-2001;
 Biotecon Diagnostics GmbH (DB)
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QY 1 CCAAGTCAACAACTGTTGT 21
 Db 1 CCAGTCACACAAGTAGTTGT 21

Db
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 LOCUS AX105729 Sequence 1 from Patent WO0123605.
 DEFINITION 267 bp DNA linear PAT 30-APR-2001
 ACCESSION AX105729
 VERSION AX105729.1 GI:13921742
 KEYWORDS
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 SOURCE Lactobacillus brevis
 ORGANISM Lactobacillus; Firmicutes; Lactobacillales; Lactobacillaceae;
 Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus.

REFERENCE 1.
 AUTHORS Fandke,M., Gusch,A. and Berghof,K.
 TITLE Method and nucleic acids for determining the presence of
 micro-organisms specific to the brewing process
 JOURNAL Patent: WO 0123605-A 1 05-APR-2001;
 Biotecon Diagnostics GmbH (DB)
 FEATURES Location/Qualifiers
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 DEFINITION U89789
 ACCESSION U89789.1 GI:1890113
 VERSION .
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 ORGANISM Calliphora vicina
 Calliphora vicina
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 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Oestroidea; Calliphoridae; Calliphora.
 REFERENCE 1.
 AUTHORS Burnmaster,T., Kolling,C., Schroer,B. and Scheller,K.
 TITLE Complete sequence, expression, and evolution of the hexamerin LSP-2
 of Calliphora vicina
 JOURNAL Insect Biochem. Mol. Biol. 28 (1), 11-22 (1998)
 MEDLINE 98215882
 PUBMED 9612935
 2. (bases 1 to 2215)
 Scheller,K., Koelling,C., Schroer,B. and Burnmaster,T.
 Direct Submission
 Submitted (17-FEB-1997) Biologie du Developpement, Institut Jacques
 Monod, 2 place Jussieu, Paris 75005, France
 FEATURES Location/Qualifiers
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 SDDDFTWVSYRTTYELVKMDMANSDDKFPPLNQDEAKCGVQPRIMLRKGKQGMP
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QY 1 CCAAGTCAACACTGTTGT 18
 Db 1687 CCAGTCACACAAGTAGT 1670

Db
 RESULT 4
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 DEFINITION 836 bp DNA linear PLN 06-JUN-2001
 ACCESSION AF149254
 VERSION AF149254.1 GI:14317917
 KEYWORDS SOURCE Brassica napus (rape)
 ORGANISM Brassica napus

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 164.027 Seconds
(without alignments)

6054.391 Million cell updates/sec

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Searched: 4526729 seqs, 2364849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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8	19.4	92.4	4693	5 AX327394 Basileute
9	19.4	92.4	4693	5 AX327399 Basileute
10	19.4	92.4	4693	5 AX327400 Basileute
11	19.4	92.4	4693	5 AX327401 Basileute
12	19.4	92.4	4694	5 AX327397 Basileute
13	19.4	92.4	4695	5 AX327392 Basileute
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C	15	18	85.7	2215 3 U89789 Calliprora
15	17.8	84.8	394 5 AX275856 Coeligena	
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18	17.8	84.8	1020 5 AF197831 Cicinnurus	
19	17.8	84.8	1020 5 AF197866 Myzomela	

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description	ORIGIN	DEFINITION	ACCESSION	VERSION	SOURCE	ORGANISM
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2	21	100.0	267	6 AX105729 Sequence AX105729	Best Local Similarity	100.0%; Pred. No. 19;				Coturnix coturnix
3	19.4	92.4	4692	5 AX327391 Basileute	Matches	21; Conservative				Accipiter nisus
4	19.4	92.4	4692	5 AX327393 Basileute						Accipiter cooperii
5	19.4	92.4	4692	5 AX327795 Basileute						Accipiter gentilis
6	19.4	92.4	4692	5 AX327392 Basileute						Accipiter striatus
7	19.4	92.4	4692	5 AX327398 Basileute						Accipiter badius
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9	19.4	92.4	4693	5 AX327399 Basileute						Accipiter cooperii
10	19.4	92.4	4693	5 AX327400 Basileute						Accipiter cooperii
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13	19.4	92.4	4695	5 AX327392 Basileute						Accipiter cooperii
14	19.4	92.4	4696	5 AX327389 Dendroica						Accipiter cooperii
C	15	18	85.7	2215 3 U89789 Calliprora						Accipiter cooperii
15	17.8	84.8	394 5 AX275856 Coeligena							Accipiter cooperii
17	17.8	84.8	1020 5 AF197830 Diphylid							Accipiter cooperii
18	17.8	84.8	1020 5 AF197831 Cicinnurus							Accipiter cooperii
19	17.8	84.8	1020 5 AF197866 Myzomela							Accipiter cooperii

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GenCore version 5.1.6

Om nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:50:19 ; Search time 34.5345 Seconds

3127.876 Million cell updates/sec

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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SUMMARIES

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5	17	85.0	12767	17 US-10-322-281-797	Sequence 197, Appli
6	15.8	84.0	175561	14 US-10-017-21-3	Sequence 3, Appli
7	16.8	84.0	175561	16 US-10-255-192-48	Sequence 48, Appli
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9	16.8	84.0	1503841	9 US-09-795-668-1	Sequence 1, Appli
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; Sequence 1, Application US/09795061
; Publication No. US20030166842A1
; GENERAL INFORMATION:
; APPLICANT: Greenpan, Daniel S
; APPLICANT: Imamure, Yasutada
; TITLE OF INVENTION: Pro-AlphA 3 (V) Collagen Genes
; FILE REFERENCE: 960295_967611
; CURRENT APPLICATION NUMBER: US/09/795, 061
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (62)..(5298)
; US-09-795-061-1

Query Match 92.0%; Score 18.4; DB 10; Length 6109;
Best Local Similarity 95.0%; Pred. No. 31;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAGGGAGAGGTCTCTTAT 20
DQ 4907 GAGGGAGAGGTCTCTTAT 4926

RESULT 2
US-10-425-115-45008
; Sequence 45008, Application US/10425115
; Publication No. US20040214272A1

GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yinhua
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21-(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO: 43008
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: MRT4577_141051C.1
; FEATURE: ;
; OTHER INFORMATION: DB 439 GGGAAAGAAGTTCTCTAT 456

RESULT 3
US-10-029-386-1346
; Sequence 1346, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS TWO
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEONICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Armonax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 1346
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: ;
; OTHER INFORMATION: MAP TO AC013816.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.43
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.46
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.36
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
; OTHER INFORMATION: SWISSPROT HIT: Q00083, EVALUE 5.80e+00
; OTHER INFORMATION: EST HUMAN HIT: SG339472.1, EVALUE 8.30e-01
; OTHER INFORMATION: NT HIT: AJ314911.1, EVALUE 2.20e+00
; US-10-029-386-1346

Query Match 87.0%; Score 17.4; DB 15; Length 553;
Best Local Similarity 94.7%; Pred. No. 74; Mismatches 1; Indels 0; Gaps 0;
Matches 18; Conservative 0; Misnmatches 1; Indels 0; Gaps 0;

Qy 2 AGGGAGAGGTCTCTAT 20
Db 524 AGGGAGAGGTCTCTAT 542

RESULT 4
US-09-795-061-3
; Sequence 3, Application US/09795061
; Publication No. US20030166842A1

RESULT 5
US-10-322-281-797
; Sequence 797, Application US/10322281
; Publication No. US20040126782A1
; GENERAL INFORMATION:
; APPLICANT: Marz, S. Malandro
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 52945201000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 797
; LENGTH: 127767
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE: ;
; NAME/KEY: misc_feature
; LOCATION: (1)..(127767)
; OTHER INFORMATION: n = A,T,C or G

US-10-322-281-797

Query Match 85.0%; Score 17; DB 17; Length 127767;
Best Local Similarity 100%; Pred. No. 2.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 0; Misnmatches 0; Indels 0; Gaps 0;

Qy 4 GCGAGAGGTCTCTAT 20
Db 5129 GGAGAGGTCTCTAT 5145

RESULT 6
US-10-017-721-3/C
; Sequence 3, Application US/10017721
; Publication No. US20030096248A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; APPLICANT: Daley, George
; APPLICANT: Boik, Stacey
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MNT-03
; CURRENT APPLICATION NUMBER: US/10/017,721
; CURRENT FILING DATE: 2001-12-14
; PRIORITY APPLICATION NUMBER: US 60/317,033
; PRIORITY FILING DATE: 2001-09-04

SUMMARIES

Copyright (C) 1993 - 2004 Compugen Ltd.
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 (without alignments)
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Sequence: 1 gagggaagaagtctctttat 20
Scoring table: IDENTITY-NUC
 Gapop 10.0 , Gapext 1.0
Searched: 824507 seqs, 35539441 residues
Total number of hits satisfying chosen parameters: 1649014
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First: 45 summaries
Database :
 Issued_Patents_NA.*
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 2: /cgn2_6/podata/1/ina/5B_COMB.seq:*
 3: /cgn2_6/podata/1/ina/61_COMB.seq:*
 4: /cgn2_6/podata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/podata/1/ina/PCITS_COMB.seq:*
 6: /cgn2_6/podata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENT

```

Sequence 1, Appli
Sequence 2, Appli
Sequence 5, Appli
Sequence 3, Appli
Sequence 556, Appli
Sequence 11, Appli
Sequence 1366, Appli
Sequence 38, Appli
Sequence 139, Appli
Sequence 11, Appli
Sequence 1245, Appli
Sequence 17, Appli
Sequence 19, Appli
Sequence 21, Appli
Sequence 23, Appli
Sequence 25, Appli
Sequence 27, Appli
Sequence 29, Appli

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; LOCATION: (87) .. (5321)
US-09-795-061-3

Query Match Score 17.4; DB 4; Length 6200;
 Best Local Similarity 94.7%; Pred. No. 18;
 Matches 18; Conservatory 94.7%; 0; Mismatches
 Oy 1 GAGGGAGAAGTCTTA 19
 Db 4927 GAGGGAGAAGTCTTA 4945

RESULT 3
 US-09-198452A-1/c
 Sequence 1, Application US/09198452A
 Patent NO. 659294
 GENERAL INFORMATION:
 APPLICANT: Griffais, R.
 TITLE OF INVENTION: chlamydia pneumoniae genomic sequence and polypeptides, fragments
 TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
 TITLE OF INVENTION: and treatment of infection
 FILE REFERENCE: 9710-003-999
 CURRENT APPLICATION NUMBER: US/09/198,452A
 CURRENT FILING DATE: 1998-11-24
 NUMBER OF SEQ ID NOS: 6949
 SEQ ID NO 1
 LENGTH: 1230025

FEATURE:
 NAME/KEY: misc feature
 LOCATION: (1)..(15000)
 OTHER INFORMATION: n=a or c or g or t
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 OTHER INFORMATION: n=a or c or g or t
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 LOCATION: (555001)..(570000)
 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc feature
 LOCATION: (570001)..(585000)

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 38.7988 Seconds
(without alignments)

US-10-088-666-74
Sequence: 1 gagggagaaggttctcttat 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: N_Geneseq_23sep04;*
- 2: geneseqn1980s;*
- 3: geneseqn2000s;*
- 4: geneseqn2001as;*
- 5: geneseqn2001bs;*
- 6: geneseqn2002as;*
- 7: geneseqn2002bs;*
- 8: geneseqn2003as;*
- 9: geneseqn2003bs;*
- 10: geneseqn2003as;*
- 11: geneseqn2003bs;*
- 12: geneseqn2004as;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
ID AA61639
XX AA61639 standard; DNA; 20 BP.
AC AA61639;
XX
DT 02-JUL-2001 (first entry)
DE Lactobacillus brevis 23S rRNA/5S rRNA specific probe SEQ ID 74.
KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
XX
OS Lactobacillus brevis.
XX
PN DE1994964-A1.
XX
PD 05-APR-2001.
XX
PF 24-SEP-1999; 99DE-01045964.
XX
PR 24-SEP-1999; 99DE-01045964.
PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
PI Fandke M., Gasch A., Berghof K.;
XX
DR WPI; 2001-246136/26.

Detecting contaminating microorganisms in brewing, by nucleic acid amplification and hybridization, either non-specific or genus- or species specific.

Claim 9(i); Page 17; 48pp; German.

This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 156.216 Seconds
(without alignments) 6054.391 Million cell updates/sec

Title: US-10-088-666-74
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Sequence: 1 gagggagaagaatctcttat 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 2364189745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
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2: gb_hg:
3: gb_in:
4: gb_om:
5: gb_or:
6: gb_patt:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_yr:
1:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1	AXI05802	AXI05802	AXI05802	Sequence 74 from Patent WO0123605.	20 bp	DNA	linear	PAT 30-APR-2001
DEFINITION									
ACCESSION									
VERSION									
KEYWORDS									
SOURCE									
ORGANISM									
ARTIFICIAL									
SEQUENCES									
REFERENCE	1								
AUTHORS	Fandke, M., Gasch, A. and Berghoff, K.								
TITLE	Method and nucleic acids for determining the presence of micro-organisms specific to the brewing process								
JOURNAL	Patent: WO 0123605-A 74-05-APR-2001;								
FEATURES									
SOURCE	Biotecon Diagnostics GmbH (DE) Location/Qualifiers								
	1..20								
	/note="spezifische Sequenz fur Lactobacillus brevis"								
	/mol_type="unassigned DNA"								
	/db_xref=ttaxon:32630"								

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description	ORIGIN
1	20	100.0	20	6	AXI05802	AXI05802 Sequence AXI05729 Sequence CQ55603 Sequence AF272661 Rattus no	
2	20	100.0	267	6	AXI05729	Query Match Similarity 100.0%; Score 20; DB 6; Length 20; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
3	18.4	92.0	337	6	AC102821	AF176645 Mus muscu AC102821 Mus muscu AC122484 Mus muscu AC117613 Mus muscu CQ23784 Sequence AXI39613 Sequence AXI05729	
4	18.4	92.0	6076	10	AC102821	Query 1 gagggagaagaatctcttat 20 Db 1 gagggagaagaatctcttat 20	
5	18.4	92.0	6109	6	AC102821		
6	18.4	92.0	6109	10	AC102821		
7	18.4	92.0	155793	10	AC102821		
8	18.4	92.0	162757	10	AC122484		
9	18.4	92.0	229813	2	AC117613		
10	17.4	87.0	1907	6	CQ23784		
11	17.4	87.0	6200	6	AC239613		
12	17.4	87.0	6200	9	AF177941		
13	17.4	87.0	6368	6	AX405643		
14	17.4	87.0	39969	9	HSJ645119		
15	17.4	87.0	110000	2	AC10925_0		
16	17.4	87.0	157410	2	AC01816		
17	17.4	87.0	165701	2	AC01457		
18	17.4	87.0	167711	9	AC00616		
19	17.4	87.0	168119	2	AC068686		

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Om nucleic - nucleic search, using sw model

Run on:

November 15, 2004, 11:05:13 ; Search time 417.042 Seconds

(without alignments)
2184.416 Million cell updates/sec

Title: `score:
Perfect score:
Sequence:

US-10-088-666-73
25
1 tsgagatataatgtatataatccatg 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
C 1	20.8	83.2	717 9 AG2296763	AG2296763 Mus muscu
C 2	20.2	80.8	460 8 AQ489622	AQ489622 RPCI-11-2
C 3	19.8	79.2	887 9 CN960955	AL417999 T3 end of AZ683885 ANTIP32TF
C 4	19.4	77.6	848 8 AZ683895	CC141515 NDL_32K2.
C 5	19.4	77.6	877 8 CCI41515	BH133066 ENTIC66TR
C 6	19.4	77.6	898 8 BH133066	BH147215 ENTOP41TR
C 7	19.4	77.6	900 8 BH147215	BH147215 ENTOP41TR
C 8	19.4	77.6	903 8 BH13872	BH13872 ENTOP41TR
C 9	19.2	76.8	214 9 CR398469	CR398469 Arabidops
C 10	19.2	76.8	277 9 CG148828	CG148828 PUFKV46TR
C 11	19.2	76.8	307 9 CII57264	CII57264 ZIMBBB061
C 12	19.2	76.8	340 6 CD324627	CD324627 Strep537.
C 13	19.2	76.8	382 9 CR3401158	CR3401158 tigr-gss-
C 14	19.2	76.8	385 9 CR324663	CR324663 tigr-gss-
C 15	19.2	76.8	390 8 BZ632366	BZ632366 PRBA54TR
C 16	19.2	76.8	405 9 CG148831	CG148831 PUFKV46TR
C 17	19.2	76.8	409 9 BZ632364	BZ632364 PRAT41TR
C 18	19.2	76.8	413 8 BZ632362	BZ632362 PRBA54TR
C 19	19.2	76.8	418 8 BZ632408	BZ632408 PRAT41TR
C 20	19.2	76.8	424 7 BH170927	BH170927 SALK_0035
C 21	19.2	76.8	464 9 CR385368	CR385368 tigr-gss-
C 22	19.2	76.8	482 7 CO517136	CO517136 s1qsg29H
C 23	19.2	76.8	568 9 CR345622	CR345622 tigr-gss-
C 24	19.2	76.8	570 9 CE313026	CE313026 tigr-gss-

ALIGNMENTS

c 25	19.2	76.8	583 9 CE029479	CE029479 tigr-gss-
c 26	19.2	76.8	601 9 CE178676	CE178676 tigr-gss-
c 27	19.2	76.8	630 9 CE407283	CE407283 tigr-gss-
c 28	19.2	76.8	639 9 CE397029	CE397029 tigr-gss-
c 29	19.2	76.8	646 9 CE717195	CE717195 tigr-gss-
c 30	19.2	76.8	685 9 CE45551	CE45551 tigr-gss-
c 31	19.2	76.8	709 9 CL827541	CL827541 OR CRa004
c 32	19.2	76.8	711 9 AG123355	AG123355 Pan trogl
c 33	19.2	76.8	713 9 CG59772	CG59772 tigr-gss-
c 34	19.2	76.8	742 9 CE224657	CE224657 tigr-gss-
c 35	19.2	76.8	757 9 CL77754	CL77754 OR BA012
c 36	19.2	76.8	833 9 CG048515	CG048515 PUT0607B
c 37	19.2	76.8	911 8 BZ829021	BZ829021 RUEQ27D
c 38	19.2	76.8	888 9 CG365204	CG365204 MBMD88TP
c 39	18.8	75.2	402 8 AQ207867	AQ207867 HS_3138_A
c 40	18.8	75.2	405 1 AI72073	AI72073 tZ1g11.x
c 41	18.8	75.2	506 9 CG656733	CG656733 MUGQ_CH25
c 42	18.8	75.2	574 8 AQ466749	AQ466749 HS_5170
c 43	18.8	75.2	595 9 CE163486	CE163486 tigr-gss-
c 44	18.8	75.2	628 6 CD046668	CD046668 VTA040E09
c 45	18.8	75.2	630 9 CR323914	CR323914 Medicago

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CE397029 tigr-gss-
CE717195 tigr-gss-
CE45551 tigr-gss-
CL827541 OR CRa004
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CG59772 tigr-gss-
CE224657 tigr-gss-
CL77754 OR BA012
CG048515 PUT0607B
BZ829021 RUEQ27D
CG365204 MBMD88TP
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AI72073 tZ1g11.x
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CD046668 VTA040E09
CR323914 Medicago

RESULT 1
AG229673/c

LOCUS AG229673 Mus musculus molossinus DNA, clone:MSMg01-073H13.T7, genomic survey sequence.
DEFINITION Mus musculus molossinus
ACCESSION AG229673
VERSION AG229673.1 GI:47869717
KEYWORDS GSS,
SOURCE Mus musculus molossinus
ORGANISM Mus musculus molossinus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Buteleostomi;
Bikarya; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

JOURNAL BAC end Sequences of Library MSMg01
REMARKS Unpublished
2 (bases 1 to 717)

Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-Nov-2003) Masahiro Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
COMMENT 1-7-22 Shiroi-chou,Tsurumi-ku, Yokohama, Kanagawa 220-0045, Japan
(E-mail:hattori@gscreiken.jp, URL: http://hgcp.gsc.riken.go.jp/; Tel: +81-45-503-9111, Fax: +81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kunuya Abe (abe@rc.riken.jp).

Tsukuba Institute, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyodai, Tsukuba, Ibaraki, Japan
Phone: +81-29-36-9189, fax: +81-298-36-9199
e-mail: abe@rc.riken.jp

PRIMERS Sequencing : T7
LIBRARY Vector : PBACE3.6
R.Site 1 : ECORI
R.Site 2 : BCOI

FEATURES location/Qualifiers source
1. .717
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
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/db_xref="taxon:5786"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_id="MSMg01-073H13.T7"

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CII57264 ZIMBBB061
CD324627 Strep537.
CR3401158 tigr-gss-
CB324663 tigr-gss-
BZ632366 PRBA54TR
CG148831 PUFKV46TR
BZ632364 PRAT41TR
BZ632362 PRBA54TR
BZ632362 PRAT41TR
BZ632408 PRAT41TR
BH170927 SALK_0035
CR385368 tigr-gss-
CO517136 s1qsg29H
CR345622 tigr-gss-
CE313026 tigr-gss-

ORIGIN		ACCESSION		AL417999	
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Best Local Similarity		KEYWORDS		GSS	
Matches	22; Conservative	0;	Mismatches	2;	Pichia farinosa
Qy	1	TGGAGATAATGAAATATCTA	24	ORGANISM	Pichia farinosa
Db	507	TCGAGATAATGAAATATCTA	484	REFERENCE	Saccharomycetales; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Fungi; Ascomycota; Saccharomycetaceae; Pichia.
RESULT	2			AUTHORS	Souillet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Casaregola, S., Bolotin, Fukuhara, M., Bon, E., Brotier, P., Lepingle, A., Llorente, B., de Montigny, J., Dujon, B., Durrieu, P., Lepingle, A., Llorente, B., Malpertuy, A., Neveuville, C., Ozier-Kalogeropoulos, O., Potier, S., Saurin, W., Tekala, F., Toffano-Nioche, C., Wesolowski-Louvel, M., Wincker, P. and Weissbach, J.
AQ489622/c		AQ489622	460 bp	ORGANISM	Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
LOCUS		RPCI-11-231C16.TV	DNA	TITLE	FEMS Lett. 487 (1), 3-12 (2000)
DEFINITION		RPCI-11-231C16, genomic survey sequence.	linear	JOURNAL	20584711
ACCESSION		AQ489622	GSS	VERSION	21152876
VERSION		AQ489622.1		AUTHORS	(bases 1 to 887)
KEYWORDS		GSS,		REFERENCE	de Montigny, J., Souillet, J., Tekala, F., Dujon, B., Wincker, P., Artiguenave, F. and Potier, S.
SOURCE		Homo sapiens (human)		JOURNAL	FEMS Lett. 487 (1), 87-90 (2000)
ORGANISM				MEDLINE	20584725
JOURNAL				PUBLISHED	11152890
COMMENT		Unpublished		REFERENCE	3 (bases 1 to 887)
REFERENCE		Other GSS: RPCI-11-231C16.TV		JOURNAL	Map Building (1997)
AUTHORS		Contact: Shaving Zhao, William Nierman, Mark Adams		COMMENT	Map Building (1997)
TITLE		1 (bases 1 to 460)		AUTHORS	Direct Submission
		Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong P. and Venter,J.C.		COMMENT	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
		Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready		REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
		Map Building (1997)		JOURNAL	Genoscope
		Other GSS: RPCI-11-231C16.TV		COMMENT	Centre National de Séquençage
		Contact: Shaving Zhao, William Nierman, Mark Adams		AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
		1 (bases 1 to 460)		REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
FEATURES		source		JOURNAL	Genoscope
		Location/Qualifiers		COMMENT	Centre National de Séquençage
		1. . 460		AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
		/organism="Homo sapiens"		REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
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		/mol_type="genomic DNA"		COMMENT	Centre National de Séquençage
		/db_xref="GDB:7588383"		AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
		/db_xref="taxon:9605"		REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
		/clone="RPCI-11-231C16"		JOURNAL	Genoscope
		/sex="Male"		COMMENT	Centre National de Séquençage
		/cell_type="Lymphocytes"		AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
		/clone_id="RPCI-11"		REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
		/note="Vector: pBAC3.6; Site_1: ECORI; Site_2: ECORI;"		JOURNAL	Genoscope
		RPCII Human Male BAC Library		COMMENT	Centre National de Séquençage
				AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
ORIGIN				REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
Query		Query Match	80.8%	JOURNAL	Genoscope
		Best Local Similarity	88.0%	COMMENT	Centre National de Séquençage
		Matches	22; Conservative	AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
RESULT	3	1	TCGAGATAATGAAATATCTAG	REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
LOCUS	CNS06W5/c	CNS06W55	887 bp	JOURNAL	Genoscope
DEFINITION		end of clone AX01M028C03 of library AX00A from strain CBS 7064		COMMENT	Centre National de Séquençage
		of <i>Pichia farinosa</i> , genomic survey sequence.		AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
RESULT	4	A2633885		REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
LOCUS		A2633885		JOURNAL	Genoscope
DEFINITION		ENTLP2TF Entamoeba histolytica Sheared DNA Entamoeba histolytica		COMMENT	Centre National de Séquençage
ACCESSION		A2683885		AUTHORS	Submitted (08-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5006, 91057 EVRY cedex, FRANCE. (E-mail: segrég@genoscope.cnrs.fr - Web : www.genoscope.cnrs.fr)
VERSION		A2683885.1		REFERENCE	This GSS is part of a random genomic sequencing program of thirteen yeast species: <i>Saccharomyces bayanus</i> var. <i>varatum</i> , <i>Saccharomyces exiguum</i> , <i>Saccharomyces kluyveri</i> , <i>Kluyveromyces thermotolerans</i> , <i>Kluyveromyces lactis</i> var. <i>lactis</i> , <i>Kluyveromyces marxianus</i> var. <i>marxianus</i> , <i>Pichia angusta</i> , <i>Debaryomyces hansenii</i> var. <i>hansenii</i> , <i>Pichia sorbitophila</i> , <i>Candida tropicalis</i> and <i>Yarrowia lipolytica</i> . Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.
SOURCE		Entamoeba histolytica		JOURNAL	Genoscope
ORGANISM		Entamoeba histolytica		COMMENT	Centre National de Séquençage

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:50:19 ; Search time 43.1682 Seconds
(without alignments)
3127.876 Million cell updates/sec

Title: US-10-088-666-73
Perfect score: 25
Sequence: 1 tcgaaaataatcgaaataatacttag 25

Scoring table: IDENTITY_NUC
GapOp 10.0 , GapExt 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum Match 0%
Maximum Match 100%
Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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 2: /cgn2_6/ptodata/2/pubpna/pct_new_pub.seq: *
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 21: /cgn2_6/ptodata/2/pubpna/us60_pubcomb.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	18.8	75.2	228	14	US-10-016-349A-108
2	18.8	75.2	1324	14	US-10-016-349A-109
3	18.6	74.4	1206	18	US-10-425-115-119404
4	18.4	73.6	1891	17	US-10-427-963-45894
5	18.2	72.8	332	15	US-10-369-93-29816
6	18.2	72.8	588	15	US-10-029-3846-6066
7	18.2	72.8	638	17	US-10-767-701-26220
8	18.2	72.8	2179	9	US-03-070-9274-468
9	18.2	72.8	163701	17	US-10-322-281-439
10	18.2	72.8	1830121	14	US-10-329-960-439
11	18.2	72.8	1830121	16	US-10-329-670-1
12	18.2	72.8	1830121	18	US-10-158-865-1

RESULT 1
US-10-016-349A-108
; Sequence 108, Application US/10016349A
; Publication No. US20030064378A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Liu, Chenghua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods relating to Lung Specific Genes and Proteins
; FILE REFERENCE: DEX-0243
; CURRENT APPLICATION NUMBER: US/10-016-349A
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/243, 459
; NUMBER OF SEQ ID NOS: 244
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 108
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-016-349A-108
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Best Local Similarity 90.9%; Pred. No. 1e+03;
Matches 20; Conservatism 0; Mismatches 2; Indels 0; Gaps 0;

Qry 4 AGATATTGATAATACTTAC 25
Db 17 AGATATTGATAATACTTAC 38

RESULT 2
US-10-016-349A-109/c

; Sequence 109, Application US/10016349A
; Publication No. US20030064378A1
; GENERAL INFORMATION:
; APPLICANT: Recipon, Herve
; APPLICANT: Sun, Yongming
; APPLICANT: Chen, Shih-Yu
; APPLICANT: Liu, Changhua
; APPLICANT: Turner, Leah
; TITLE OF INVENTION: Compositions and Methods relating to Lung Specific Genes and Prot
; FILE REFERENCE: DEX-0243
; CURRENT APPLICATION NUMBER: US/10/0163,349A
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/243,459
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO: 109
; TYPE: DNA
; ORGANISM: Homo sapiens
; LENGTH: 1324
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; LOCATION: (312)..(312)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (385)..(385)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (419)..(419)
; OTHER INFORMATION: n = a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (517)..(518)
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; LOCATION: (506)..(506)
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (419)..(419)
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; Best Local Similarity 90.9%; Pred. No. 1.2e+03; Mismatches 2;
; Matches 20; Conservative 0; N mismatches 2;
; Indels 0; Gaps 0;
; Db 1224 AGATGATTGATAGTACAG 1203
; RESULT 3
; US-10-425-115-119404/c
; Sequence 119404, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yinhua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21/53221B
; CURRENT APPLICATION NUMBER: US10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO: 45994
; LENGTH: 1891
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48814C.1
; US-10-437-963-45894
; Query Match 73.6%; Score 18.4; DB 17; Length 1891;
; Best Local Similarity 95.0%; Pred. No. 1.8e+03; Mismatches 1; Indels 0; Gaps 0;
; Matches 19; Conservative 0; N mismatches 1;
; Indels 0; Gaps 0;
; Db 1795 ACAATATTGATATACT 1776
; RESULT 5
; US-10-369-493-29816/c
; Sequence 29816, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10/520521B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/3360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO: 29816
; LENGTH: 332
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
; Query Match 72.8%; Score 18.2; DB 15; Length 332;
; Best Local Similarity 87.0%; Pred. No. 1.8e+03; Mismatches 3;
; Matches 20; Conservative 0; N mismatches 3;
; Indels 0; Gaps 0;
; US-10-369-493-59816
; Query Match 72.8%; Score 18.2; DB 15; Length 332;
; Best Local Similarity 87.0%; Pred. No. 1.8e+03; Mismatches 3;
; Matches 20; Conservative 0; N mismatches 3;
; Indels 0; Gaps 0;

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

Om nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:14 ; Search time 10.8108 Seconds
(without alignments)
1643.699 Million cell updates/sec

Title: US-10-088-666-73
Perfect score: 25
Sequence: 1 to gagaataattgaaataatcttag 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NL: *
1: /cgn2_6/podata/lina/5A-COMB.seq: *
2: /cgn2_6/podata/lina/5B-COMB.seq: *
3: /cgn2_6/podata/lina/5C-COMB.seq: *
4: /cgn2_6/podata/lina/6B-COMB.seq: *
5: /cgn2_6/podata/lina/PCUTS-COMB.seq: *
6: /cgn2_6/podata/lina/rackfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query Match Length	DB ID	Description
C 1	18.4	73.6	5064	4 US-08-936-107A-8 Sequence 8, Appli
C 2	18.2	72.6	234	4 US-08-936-107A-8 Sequence 317, Appli
C 3	18.2	72.8	468	4 US-08-134-000C-316 Sequence 316, Appli
C 4	18.2	72.8	1830121	4 US-09-557-884-1 Sequence 1, Appli
C 5	18.2	72.8	1830121	4 US-09-643-910A-1 Sequence 1, Appli
C 6	18.2	72.8	1830121	4 US-10-326-960-1 Sequence 1, Appli
C 7	17.6	70.4	103	4 US-09-313-294A-1738 Sequence 1738, Appli
C 8	17.6	70.4	210	4 US-09-313-294A-1738 Sequence 2255, Appli
C 9	17.6	70.4	1001	4 US-09-641-638-111 Sequence 111, Appli
C 10	17.6	70.4	1001	4 US-09-641-638-112 Sequence 112, Appli
C 11	17.6	70.4	1001	4 US-09-170-097-111 Sequence 111, Appli
C 12	17.6	70.4	1001	4 US-11-170-097-112 Sequence 112, Appli
C 13	17.4	69.6	1830121	4 US-09-557-884-1 Sequence 1, Appli
C 14	17.4	69.6	1830121	4 US-09-643-910A-1 Sequence 1, Appli
C 15	17.4	69.6	1830121	4 US-10-329-960-1 Sequence 1, Appli
C 16	17.2	68.8	441	4 US-09-102-919-1795 Sequence 1795, Appli
C 17	17.2	68.8	462	3 US-03-134-001C-2294 Sequence 2294, Appli
C 18	17.2	68.8	2943	4 US-03-710-279-3983 Sequence 3983, Appli
C 19	17.2	68.8	3249	4 US-09-711-279-3622 Sequence 3622, Appli
C 20	17.2	68.8	3442	4 US-09-710-279-4030 Sequence 4030, Appli
C 21	17	68.0	1557	4 US-03-270-767-2896 Sequence 28519, Appli
C 22	17	68.0	1907	4 US-09-270-767-13100 Sequence 13100, Appli
C 23	17	68.0	2970	4 US-09-710-279-2593 Sequence 2593, Appli
C 24	17	68.0	3128	4 US-03-270-767-12506 Sequence 12706, Appli
C 25	17	68.0	3271	4 US-09-710-279-4142 Sequence 4142, Appli
C 26	17	68.0	3461	4 US-09-710-279-3713 Sequence 3713, Appli

ALIGNMENTS

RESULT 1
US-08-936-107A-8/C
Sequence 8, Application US/08936107A
Patent No. 6403306

GENERAL INFORMATION:

APPLICANT: Stephens, David S.
ATTORNEY: Swartley, John S.

TITLE OF INVENTION: Serogroup-Specific Nucleotide Sequences in the Molecular Typing of Bacterial Isolates and the Preparation of Vaccines Thereof

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936, 107A
FILING DATE: 23-SEP-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/827, 622
FILING DATE: 09-APR-1997

ATTORNEY/AGENT INFORMATION:
NAME: Cruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERRED DOCKET NUMBER: 77-97

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8059

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 5064 base pairs

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 479..1597
FEATURE:
NAME/KEY: CDS

LOCATION: 1599..3235
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 3309..4052
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 4054..4917
 US-08-936-107A-8

Query Match Similarity 73.6%; Score 18 4; DB 4; Length 5064;
 Best Local Similarity 95.0%; Pred. No. 86; Mismatches 1; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 2
 US-05-134-000C-317
 Sequence 317 Application US/09134000C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 317
 LENGTH: 234
 TYPE: DNA
 ORGANISM: Enterococcus faecalis

US-05-134-000C-317
 Query Match Similarity 72.8%; Score 18 2; DB 4; Length 234;
 Best Local Similarity 87.0%; Pred. No. 1..e-02; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGAGATAATGAAATCTA 20
 Db 3612 TCGATAATAATGAAATAA 3593

RESULT 3
 US-05-134-000C-316/c
 Sequence 316 Application US/09134000C
 Patent No. 6617156
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134,000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 316
 LENGTH: 468
 TYPE: DNA
 ORGANISM: Enterococcus faecalis

US-09-134-000C-316
 Query Match Similarity 72.8%; Score 18.2; DB 4; Length 468;
 Best Local Similarity 87.0%; Pred. No. 1.e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-09-557-884-1
 Sequence 1 Application US/09557884
 Patent No. 6506581
 GENERAL INFORMATION:
 APPLICANT: Fleischmann et al.
 TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments
 NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: MD
 COUNTY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2 inch diskette
 COMPUTER: Dell Pentium
 OPERATING SYSTEM: MS DOS v6.22
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/557,884
 FILING DATE: 25-Apr-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/476,102
 FILING DATE: JUN-5-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Michelle S. Marks
 REGISTRATION NUMBER: 41,971
 REFERENCE DOCKET NUMBER: PBR186P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-5049
 FAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1830121 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-557-884-1

RESULT 5
 US-09-643-990A-1
 Sequence 1 Application US/09643990A
 Patent No. 6528289
 GENERAL INFORMATION:
 APPLICANT: Robert D. Fleischmann
 Mark D. Adams
 Owen White
 Hamilton O. Smith
 J. Craig Venter
 TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments
 NUMBER OF SEQUENCES: 1

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 48.4995 Seconds
(Without alignments)
2705.971 Million cell updates/sec

Title: US-10-088-666-73
Perfect score: 25
Sequence: 1 tcgagaataatgtaaaaatatctag 25

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04;*

1: geneseqn1980s;*
2: geneseqn1990s;*
3: geneseqn2000s;*
4: geneseqn2001as;*
5: geneseqn2001bs;*
6: geneseqn2002as;*
7: geneseqn2002bs;*
8: geneseqn2003as;*
9: geneseqn2003bs;*
10: geneseqn2003cs;*
11: geneseqn2003ds;*
12: geneseqn2004as;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
ID AA61638
XX AACF61638 standard; DNA; 25 BP.
AC AACF61638;
XX DT 02-JUL-2001 (first entry)

DE Lactobacillus brevis 23S rRNA/5S rRNA specific probe SEQ ID 73.

XX KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

OS Lactobacillus brevis.

XX PN DE19945964-A1.

XX PD 05-APR-2001.

XX PF 24-SEP-1999; 99DE-01045964.

XX PR 24-SEP-1999; 99DE-01045964.

XX PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX PR Fandke M, Gasch A, Berghoff K;

XX DR WPI; 2001-246136/26.

PT Detecting contaminating microorganisms in brewing, by nucleic acid amplification and hybridization, either non-specific or genus- or species specific.

PT This invention describes a novel method for detecting microorganisms (A) of importance in brewing, which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating

CC Abx83278 Corn ear-ab
Abx74381 Corn tass-ab
Abx83795 Corn ear-ab
Ab183657 Human ova
Acc57478 Arachidone
Acc57477 Arachidon
Acc39081 Arabidops
Acc33067 Prokaryot
Acc52951 Enterococ
Ab12259 Drosophil
Av03313 Archaeogl
Aal15648 Phosphata
Ab121402 Drosophil
Acc63311 Chemical
Ab12258 Drosophil
Ab13442 Human lmm
Abq67097 Human ang
Aak7255 Human imm
Axk2048 Boxlelia
Add47194 DNA seque
Add6744 Human ROC
Add3221 Human TGF
Acc53033 Haemophil
Acc34026 Prokaryot

ALIGMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	25	100.0	25 5 AAF61638	Aaf61638 Lactobaci
2	25	100.0	25 5 AAF61638	Aaf61566 Lactobaci
3	18.8	75.2	228 8 ABQ82965	Abq82965 Human lmm
4	18.8	75.2	1324 8 ABQ82966	Abq82966 Human lmm
5	18.4	73.6	5054 2 AAV69110	Aav69110 Neisseria
6	18.4	73.6	25426 8 ADA1645	Ada1645 Human sec
7	18.4	73.6	25426 8 ACC0940	Acc0940 Human sec
8	18.4	73.6	25426 10 AD38155	Ad38155 CDNA clon
9	18.4	73.6	25426 10 AD57777	Ad57777 BAC fragm
10	18.2	72.8	234 10 AD82432	Ad82432 Enterococ
11	18.2	72.8	468 10 AD82431	Ad82431 Enterococ
12	18.2	72.8	588 12 ACH2871	Ach2871 Human gen
13	18.2	72.8	2179 2 AX13405	Ax13405 Enterococ
14	18.2	72.8	2179 6 ABS9200	Ab99200 Enterococ
15	18.2	72.8	25426 10 AD57777	Ad57777 BAC fragm
16	18.2	72.8	11000 2 AAT2063_03	Aat2063_03
17	18	72.0	1190 2 AX13651_	Ax13651 Enterococ
18	18	72.0	1190 6 AB99446	Ab99446 Enterococ
19	18	72.0	5962 6 ABL33286	Ab133286 Human imm
20	17.8	71.2	1151 10 ADC08440	Adc08440 Rice DNA
21	17.8	71.2	3393 8 ABT17845	Abt17845 Aspergill

CC microbes, either as a general test for contamination or as a test specific for particular genera or (sub) species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis.

XX Sequence 25 BP; 11 A; 2 C; 4 G; 8 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.9; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db Qy 1 TCGAGAATATTGATAATATCTAG 25
1 TCGAGAATATTGATAATATCTAG 25

RESULT 2
ID AAF61566
ID AAF61566 standard; DNA; 267 BP.
XX
AC AAF61566;
XX
DT 02-JUL-2001 (first entry)
XX
DE Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.
XX
KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
XX
OS Lactobacillus brevis.
XX
PN DE19945964-A1.
XX
PD 05-APR-2001.
XX
PP 24-SEP-1999; 99DE-01045964.
PR 24-SEP-1999; 99DE-01045964.
XX
PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX
PI Fandke M, Gasch A, Berghof K;
DR WPI; 2001-246136/26.

PT Detecting contaminating microorganisms in brewing, by nucleic acid amplification and hybridization, either non-specific or genus- or species -specific.

XX
PS Claim 1; Page 9; 48pp; German.

CC This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating microbes, either as a general test for contamination or as a test specific for particular genera or (sub) species. It is quicker than known microbiological methods, and can detect several organisms in the same sample, including organisms not presently recognized as contaminants. The method provides an early indication of contamination and can be automated for high throughput analysis.

XX Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 25; DB 5; Length 267;
Best Local Similarity 100.0%; Pred. No. 2.7; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db Qy 4 AGAAATTCATGATATCTAG 25
4 AGAAATTCATGATATCTAG 25
Db 17 AGATGATGATGATCTAG 38

RESULT 3
ID ABQ82965
ID ABQ82965 standard; cDNA; 228 BP.
XX
AC ABQ82965;
XX
DT 15-JAN-2003 (first entry)
XX
DE Human lung specific nucleic acid (LSNA) SEQ ID NO:108.
XX
KW Human; lung specific protein; lung cancer; vaccine; gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200277236-A2.
XX
PD 03-OCT-2002.
XX
PF 26-OCT-2001; 2001WO-US050385.
XX
PR 26-OCT-2000; 2000US-0243459P.
XX
PA (DIAD-) DIADEXIS INC.
XX
PI Recipon H, Sun Y, Chen S, Liu C, Turner LR;
XX
DR WPI; 2003-018930/01.
XX
PT New isolated nucleic acid molecule, useful for treating lung cancer, and PT diagnosing or monitoring the presence of metastases of lung cancer in a patient.
XX
PS Claim 1; Page 204; 262PP; English.
XX
CC The present invention describes a isolated human lung specific nucleic acid (LSNA) molecule comprising a sequence selected from ABQ82858 to ABQ8293, which encodes a human lung specific protein (LSP) sequence selected from ABP515 to ABP5472. Also described: (1) a method for determining the presence of a LSNA or LSP in a sample; (2) a vector comprising the novel nucleic acid; (3) a host cell comprising the vector of (2); (4) producing a polypeptide encoded by the novel nucleic acid; (5) an isolated polypeptide produced by the method of (4); (6) an antibody or its fragment that specifically binds to the polypeptide of (5); (7) diagnosing and monitoring the presence of metastases of lung cancer in a patient; (8) treating a patient with lung cancer; or (9) a vaccine comprising the polypeptide of (5) or the novel nucleic acid. The human LSNA and LSP sequences have cytostatic activity, and can be used in vaccines and gene therapy. The LSNA and LSP sequences can also be used for treating lung cancer, and diagnosing or monitoring the presence of metastases of lung cancer, in a patient.

XX Sequence 228 BP; 83 A; 29 C; 50 G; 65 T; 0 U; 0 Other;

SQ Query Match 75.2%; Score 18.8; DB 8; Length 228;
Best Local Similarity 90.9%; Pred. No. 6e+02; Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db Qy 4 AGAAATTCATGATATCTAG 25
4 AGAAATTCATGATATCTAG 25
Db 17 AGATGATGATGATCTAG 38

RESULT 4
ID ABQ82966/c
ID ABQ82966 standard; cDNA; 1324 BP.

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(c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using SW model

Run on: November 15, 2004, 11:05:13 ; Search time 195.27 seconds
(without alignments)

6054.391 Million cell updates/sec

Title: US-10-088-666-73

Perfect score: 25

Sequence: 1 tcgagaataattgaataatctatcg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBmbl,*
1: gb_baa:*,
2: gb_lntg:*,
3: gb_jin:*,
4: gb_omn:*,
5: gb_over:*,
6: gb_patt:*,
7: gb_ph:*,
8: gb_Pl:*,
9: gb_Pri:*,
10: gb_r0:*,
11: gb_sts:*,
12: gb_EY:*,
13: gb_un:*,
14: gb_vii:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	DEFINITION	ACCESSION	SEQUENCE	LENGTH	TYPE	VERSION
RESULT 1	AXI05801	AXI05801	Sequence 73 from Patent WO0123605.	25 bp	DNA	PAT 30-APR-2001
	LOCUS					
	DEFINITION					
	ACCESSION					
	KEYWORDS					
	SOURCE					
	ORGANISM					
	artificial sequences.					
1:	Fandke,M., Gasch,A. and Berghof,K.					
	Method and nucleic acids for determining the presence of micro-organisms specific to the brewing process					
	Patent: WO 0123605-A 73 05-APR-2001;					
	FEATURES					
	SOURCE					
	Biotec Diagnostics GmbH (DB)					
	Location/(Qualifiers					
	1..25					

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	25	100.0	25 AXI05801	AXI05801 Sequence
2	25	100.0	26 AXI05729	AXI05729 Sequence
3	20.4	81.6	267 6 AC141815_0	AC141815 Apis melliferae
4	20.2	80.8	54701 2 AC079132	AC079132 Homo sapiens
5	20.2	80.8	178448 9 AC098005	AC098005 Homo sapiens
6	19.8	79.2	153768 9 AC13566	AC13566 Canis familiaris
7	19.8	79.2	238427 2 AC112334	AC112334 Canis familiaris
8	19.4	77.6	119113 5 BX005199	BX005199 Zebrafish
9	19.4	77.6	145011 2 CR48634	CR48634 Danio rerio
10	19.4	77.6	149163 2 AC079835	AC079835 Homo sapiens
11	19.4	77.6	154412 9 HS144713	HS144713 Human DNA
12	19.4	77.6	195130 9 AL559832	AL559832 Human DNA
13	19.2	76.8	482 11 CR377191	CR377191 Arabidopsis thaliana
14	19.2	76.8	1131 10 AF012235	AF012235 Cryptosporidium parvum
15	19.2	76.8	35291 5 BX649551	BX649551 Zebrafish
16	19.2	76.8	83537 5 BX0050805	BX0050805 Zebrafish
17	19.2	76.8	92624 8 AC030000	AC030000 Arabidopsis thaliana
18	19.2	76.8	102029 9 AC133537	AC133537 Homo sapiens
19	19.2	76.8	123406 8 AC120508	AC120508 Oryza sativa

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.

REFERENCE
1. Fandke, M., Gasch, A. and Berghof, K.
Method and nucleic acids for determining the presence of
micro-organisms specific to the brewing process
Patent: WO 0123605-A 1 05-APR-2001;

JOURNAL
Biotecon Diagnostics GmbH (DE)
Location/Qualifiers
1. .267
/organism="lactobacillus brevis"
/mol_type="unassigned DNA"
/db_xref="taxon:1580"

FEATURES
source

ORIGIN

Query Match	100.0%	Score	25	DB	6	Length	267
Best Local Matches	100.0%	Pred. No.	25	Indels	0	Gaps	0
25; Conservative	0	Mismatches	0				

QY
1 TCGAGATATTGAAATACTAG 25

Db
125 TCGAGATATTGAAATACTAG 149

RESULT 3
AC141815 0/c
WPOCCN

SEQUENCE split into 4 fragments
LOCUS AC141815 Accession AC141815

Fragment Name	Begin	End
AC141815_0	1	11000
AC141815_1	100001	210000
AC141815_2	200001	310000
AC141815_3	300001	409619

LOCUS AC141815 409619 bp DNA linear HTG 19-MAR-2003

DEFINITION Apis mellifera clone CH224-61C4, WORKING DRAFT SEQUENCE, 94 unorderd pieces.

ACCESSION AC141815

VERSION AC141815_1 GI:29123999

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT.

SOURCE

ORGANISM
Apis mellifera (honey bee)

REFERENCE
1. (bases 1 to 409619)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,
Aldrichos, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T.,
Barbaria, J., Benton, J., Bimage, K., Blanckenhorn, K., Bonni, D.,
Bouck, J., Bowie, S., Brevia, M., Brown, E., Brown, M., Bryant, N.P.,
Buhey, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Caron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Bathorne, S.R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.B.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
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Earnhart, C., Edgar, D., Edwards, C.C., Bhal, C., Escott, M.,
Falls, T., Ferragut, D., Flieg, N., Ford, J., Foster, P., Frantz, P.,
Gabisia, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
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Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
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Homi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E.,
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Karlsson, E., Kelly, S., Khan, U., King, J., Kovar, C., Koval, M.,
Kratovic, J., Kureishi, A., Landry, J., Leal, B., Lewis, J.C., Lewis, L.,
Li, J., Li, Z., Lichtenegger, O., Lieu, C., Liu, J., Liu, W., Lousegard, H.,
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REFERENCE
2. (bases 1 to 409619)
Worley, K.C.

SEQUENCE Direct Submission

DEFINITION Submitted (19-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu

PROJECT Project Information
Center project name: AMBL
Center clone name: CH224-61C4

STATISTICS Summary Statistics

SEQUENCING VECTOR: Plasmid;
CHEMISTRY: Dye-terminator Big Dye; 100% of reads
ASSEMBLY PROGRAM: Phrag; version 0.990329
CONSENSUS QUALITY: 37169 bases at least Q40
CONSENSUS QUALITY: 383051 bases at least Q30
CONSENSUS QUALITY: 392893 bases at least Q20
ESTIMATED INSERT SIZE: 375080; sum-of-contigs estimation
QUALITY COVERAGE: 3x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length.
(see http://www.hgsc.bcm.tmc.edu/docs/Gembank_draft_data.html)

NOTE: This sequence may represent more than one clone.

NOTE: This is a working draft sequence. It currently consists of 94 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1. 1189: contig of 1189 bp in length
1190 1189: gap of unknown length
1290 2420: contig of 1131 bp in length
2421 2520: gap of unknown length
2521 3713: contig of 1193 bp in length
3714 3813: gap of unknown length
3814 4963: contig of 1150 bp in length
4964 5063: gap of unknown length
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6388 6484: gap of unknown length
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15422 15522: gap of unknown length

Oragunwe, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, J., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rubjord, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshani, N., Sison, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamrissa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G., and Gibbs, R.
Direct Submission
Unpublished

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Om nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 350.315 Seconds
(w/o alignments) 2184.416 Million cell updates/sec

Title: US-10-088-666-21
Perfect score: 21
Sequence: 1 ccaagtcacaaacgttgtt 21

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: EST:*
- 2: gb_est1:*
- 3: gb_htc:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	18	85.7	BH542735	BH542735 BOGXU95TR
2	17.8	84.8	BFR430206	BFR430206 256171 MA
3	17.8	84.8	BH477537	BH477537 161290 BA
4	17.8	84.8	BH478105	BH478105 162195 BA
5	17.8	84.8	BH48429	BH48429 174324 BA
6	17.8	84.8	CRR383046	CRR383046
7	17.8	84.8	CF614527	CF614527 CES008733
8	17.8	84.8	AW126583	AW126583 603977 MAR
9	17.8	84.8	BH640947	BH640947 SSB-BbBc
10	17.8	84.8	BH483687	BH483687 160949 BA
11	17.8	84.8	BH476991	BH476991 1.0485 BA
12	17.8	84.8	AV613476	AV613476 AV613476
13	17.8	84.8	CF362784	CF362784 8305 MA
14	17.8	84.8	CB168898	CB168898 CW1602169
15	17.8	84.8	BFR20248	BFR20248 251764 BA
16	17.8	84.8	BH598457	BH598457 139395 BA
17	17.8	84.8	AV618453	AV618453 AVE18453
18	17.8	84.8	CB166949	CB166949 BT0602600
19	17.8	84.8	BF476579	BF476579 159906 BA
20	17.8	84.8	BE43083	BE43083 168114 BA
21	17.8	84.8	BW43873	BW43873 1DEJ7C4 a
22	17.8	84.8	BP110601	BP110601 BP110601
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27				BB483952 170440 BA
28				BM31900 1UEJ13H12
29				BB483642 169866 BA
30				BM432022 1UEJ15D6
31				BP107620 BP107620
32				BB481915 167527 BA
33				BB485555 172621 BA
34				BB482287 168021 BA
35				BB481721 167202 BA
36				BB487910 17756 BA
37				BB476202 158828 BA
38				BB480446 165528 BA
39				AV67257 AV67257
40				CF361779 827812 MA
41				BG690664 339334 BA
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45				AV606713 AV606713

ALIGNMENTS

RESULT 2				
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DEFINITION	LOCUS	Bos taurus	CDNA 5'	, mRNA sequence.
BF430206	VERSION	256171	MARC BSM	
DEFINITION	KEYWORDS			EST.
SOURCE	ORGANISM	Bos taurus	(cow)	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.			
REFERENCE	AUTHORS	1 (bases 1 to 197)		
COMMENT	Warren, W.C., Tao, N., Allison, T., Wagner, S., Mathialagan, N., Kata, S., Johnson, J., Smith, T.P.L. and Womack, J. M.			
JOURNAL	TITLE	A survey of genes transcribed in bovine skeletal muscle		
	Unpublished (2000)			
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	Matches	19; Conservative 0; Mismatches 2;		
	QY	Indels 0; Gaps 0;		
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ORIGIN				
FORWARD:	AGGAACAGCTATGACAT			
BACKWARD:	GTTTCCGAGTCAGCAGC			
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	Best Local Similarity	90.5%; Pred. No. 3.2e+02;		
	Matches	19; Conservative 0; Mismatches 2;		
	QY	Indels 0; Gaps 0;		
	Db	1 1 CCAATCTAACGTTGT 158		
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BACKWARD:	GTTTCCGAGTCAGCAGC			
FEATURES	source	Seq primer: ATTAGTAGGAGCATATAG.		
SOURCE	location/Qualifiers	Location/Qualifiers		
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BACKWARD:	GTTTCCGAGTCAGCAGC			
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BACKWARD:	GTTTCCGAGTCAGCAGC			
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Copyright (c) 1993 - 2004 GenCore version 5.1.6
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Gapop 10.0 , Gapext 1.0

ALIGNMENTS

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21: /cgn2_6_ptodata/2/pubpna/us60_PUBCOMB.seq:*

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PRED. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
US-03-960-152-4229
Sequence 4229, Application US/03960352
GENERAL INFORMATION:
Patent No. US2003013739A1
Applicant: Warren, Wesley C.
Applicant: Tao, Nembing
Applicant: Byatt, John C.
Applicant: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 1511.005/37-21(1028)C
CURRENT APPLICATION NUMBER: US/09/960, 352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO: 4229
Page: 107

GENERAL INFORMATION:
 APPLICANT: Warren, Wesley C.
 APPLICANT: Tao, Mengbing
 APPLICANT: Byatt, John C.
 APPLICANT: Mathialagan, Nagappan
 TITLE OF INVENTION: NUCLEAR ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10298)C
 CURRENT APPLICATION NUMBER: US/09/960,352
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO: 2061
 LENGTH: 211
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: Clone ID: 09-LIB34-062-Q1-E1-C9
 US-09-960-352-2061

RESULT 3
 Query Match 84.8%; Score 17.8; DB 9; Length 211;
 Best Local Similarity 90.5%; Pred. No. 62; Mismatches 2; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;
 Qy 1 CCAAGTCACAAACGGTAGTGT 21
 Db 124 CCAATCTACAAACGGTAGTGT 144

APPLICANT: Warren, Wesley C.
 APPLICANT: Tao, Mengbing
 APPLICANT: Byatt, John C.
 APPLICANT: Mathialagan, Nagappan
 APPLICANT: Mathialagan, Nagappan
 APPLICANT: Byatt, John C.
 APPLICANT: Tao, Mengbing
 APPLICANT: Byatt, John C.
 APPLICANT: Mathialagan, Nagappan
 TITLE OF INVENTION: NUCLEAR ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10298)C
 CURRENT APPLICATION NUMBER: US/09/960,352
 CURRENT FILING DATE: 2001-09-24
 NUMBER OF SEQ ID NOS: 15112
 SEQ ID NO: 4220
 LENGTH: 229
 TYPE: DNA
 ORGANISM: Bos taurus
 OTHER INFORMATION: Clone ID: 18-LIB34-051-Q1-E1-E5
 US-09-960-352-4220

Query Match 84.8%; Score 17.8; DB 9; Length 229;
 Best Local Similarity 90.5%; Pred. No. 63; Mismatches 2; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;
 Qy 1 CCAACTCAACACGGTAGTGT 21
 Db 144 CCAATCTACAAACGGTAGTGT 164

RESULT 4
 US-09-960-352-13451
 ; Sequence 13451, Application US/09960352
 ; Patent No. US20020137139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Warren, Wesley C.
 ; APPLICANT: Tao, Mengbing
 ; APPLICANT: Byatt, John C.
 ; APPLICANT: Mathialagan, Nagappan
 ; TITLE OF INVENTION: NUCLEAR ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10298)C
 ; CURRENT APPLICATION NUMBER: US/09/960,352
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 15112
 ; SEQ ID NO: 183
 ; LENGTH: 247
 ; TYPE: DNA
 ; ORGANISM: Bos taurus
 ; OTHER INFORMATION: Clone ID: 01-LIB34-051-Q1-E1-A9
 US-09-960-352-183

Query Match 84.8%; Score 17.8; DB 9; Length 247;
 Best Local Similarity 90.5%; Pred. No. 64; Mismatches 2; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;

Copyright GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:14 ; Search time 9.08108 Seconds

Title: US-10-088-666-21

Perfect score: 21

Sequence: 1 ccaagttaacaacgtagttgt 21

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NAI*

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4: /cgn2_6/podata/1/ina/6B_COMB.seq: *
5: /cgn2_6/podata/1/in/pCTUS_COMB.seq: *
6: /cgn2_6/podata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
c 1	16.2	77.1	525	4	US-09-248-796A-1527	Sequence 1527, AP
c 2	16.2	77.1	963	4	US-09-328-352-3811	Sequence 3811, AP
c 3	16.2	77.1	8878	1	US-08-759-444-2	Sequence 1, Appli
c 4	16.2	77.1	9880	3	US-08-680-897-1	Sequence 1, Appli
c 5	15.8	75.2	996	3	US-09-094-557-33	Sequence 33, Appli
c 6	15.8	75.2	1050	4	US-09-134-002-2255	Sequence 2255, AP
c 7	15.8	75.2	1053	4	US-09-071-035-409	Sequence 409, AP
c 8	15.8	75.2	2666	4	US-09-524-101D-21	Sequence 21, Appli
c 9	15.4	73.3	780	4	US-09-248-796A-6461	Sequence 6461, AP
c 10	15.4	73.3	1380	4	US-09-328-352-337	Sequence 537, AP
c 11	15.2	72.4	735	4	US-09-094-874-16	Sequence 6339, AP
c 12	15.2	72.4	1610	3	US-09-759-444-19	Sequence 19, AP
c 13	15.2	72.4	2209	4	US-09-489-847-16	Sequence 16, Appli
c 14	15.2	72.4	3070	4	US-09-799-451-652	Sequence 652, AP
c 15	15.2	72.4	13508	4	US-08-781-986A-120	Sequence 120, AP
c 16	15.2	72.4	13508	4	US-08-612-895A-97	Sequence 9, Appli
c 17	14.8	70.5	336	3	US-09-293-293-9	Sequence 9, Appli
c 18	14.8	70.5	36	3	US-09-459-553-9	Sequence 9, Appli
c 19	14.8	70.5	36	3	US-09-459-553-9	Sequence 9, Appli
c 20	14.8	70.5	36	4	US-09-882-246-9	Sequence 9, Appli
c 21	14.8	70.5	36	4	PCT-1594-10562-9	Sequence 9, Appli
c 22	14.8	70.5	5725	4	US-08-502-787A-45	Sequence 45, Appli
c 23	14.6	69.5	105	4	US-09-206-942-9	Sequence 9, Appli
c 24	14.6	69.5	127	4	US-08-781-986A-4780	Sequence 4780, AP
c 25	14.6	69.5	127	4	US-09-252-991A-6214	Sequence 6214, AP
c 26	14.6	69.5	267	4	US-08-956-171E-4419	Sequence 4419, AP
c 27	14.6	69.5	300	4	US-08-781-986A-4419	Sequence 4419, AP

ALIGNMENTS

RESULT 1
US-09-248-796A-1527/C
; Sequence 1527, Application US/09248796A
; Patent No. 6747137

GENERAL INFORMATION

APPLICANT: Keith Winstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196-132

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO: 1527

LENGTH: 525

TYPE: DNA

ORGANISM: Candida albicans

US-09-248-796A-1527

Query Match 77.1%; Score 16.2; DB 4; Length 525;

Best Local Similarity 85.7%; Pred. No. 52; Mismatches 0; Indels 3; Gaps 0;

Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Ov 1 CCCAGTCACAACTGTTGT 21

Dx 279 CCCAGTCACAACTGTTGT 259

RESULT 2
US-09-328-352-3811

GENERAL INFORMATION

APPLICANT: Gary L. Breton et al.

SEQUENCE 3811, Application US/09328352

PATENT NO. 6562958

GENERAL INFORMATION

APPLICANT: Gary L. Breton et al.

SEQUENCE 3811, Application US/09328352

PATENT NO. 6562958

GENERAL INFORMATION

APPLICANT: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTCC99-03PA

CURRENT APPLICATION NUMBER: US/19/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO: 3811

LENGTH: 963

TYPE: DNA

ORGANISM: Acinetobacter baumannii

US-09-328-352-3811

Query Match 77.1%; Score 16.2; DB 4; Length 963;

Best Local Similarity 85.7%; Pred. No. 69; Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

US-08-759-4442/c
 Sequence 2, Application US/08759444
 Patent No. 5824308

GENERAL INFORMATION:
 APPLICANT: Dassarna, Shiladitya
 ADDRESSER: Fish & Richardson, P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: US
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEC for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,444
 FILING DATE: 05-DEC-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Meiklejohn, Ph.D., Anita L
 PRIORITY APPLICATION DATA:
 REGISTRATION NUMBER: 35,283
 REFERENCE/DOCKET NUMBER: 07880/003001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-542-8906
 FAX: 617-542-8906
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8878 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-680-897-1

Query Match
 Best Local Similarity 85.7%; Pred. No. 1e+02; DB 1; Length 8878;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGTTGT 21
 Db 6765 CGAAGTACCCAGGTAGTTG 6745

RESULT 4

US-08-680-897-1/c
 Sequence 1, Application US/08680897
 Patent No. 6008051

GENERAL INFORMATION:
 APPLICANT: Dassarna, Shiladitya
 APPLICANT: Halladay, John

APPLICANT: Ng, Wan-Lip
 TITLE OF INVENTION: RECOMBINANT VECTOR AND PROCESS FOR CELL FLOTATION

NUMBER OF SEQUENCES: 1

Correspondence Address:
 ADDRESSEE: Scully, Murphy & Presser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 11530

Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-DOS/MS-DOS
 Software: PatentIn Release #1.0, Version #1.25

Current Application Data:
 Application Number: US/08/680,897
 Classification: 435
 Attorney/Agent Information:
 Name: DIGIILIO, Frank S.
 Registration Number: 31,345
 Reference/Docket Number: 8880
 Telecommunication Information:
 Telephone: (516) 742-4343
 Telex: 230 901 SANS UR
 Information for Seq ID No: 1:
 Sequence Characteristics:
 Length: 9880 base pairs
 Type: nucleic acid
 Strandedness: single
 Topology: linear
 Molecular Type: DNA (genomic)

US-09-094-557-33

Query Match
 Best Local Similarity 85.7%; Pred. No. 1e+02; DB 3; Length 9880;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCAAGTCACACGTTGT 21
 Db 7765 CGAAGTACCCAGGTAGTTG 7745

RESULT 5

US-09-094-557-33

Sequence 33, Application US/09094557
 Patent No. 6225531

General Information:
 Applicant: Kakitani, Makoto
 Applicant: Umemoto, Naoyuki
 Applicant: Ishida, Isao
 Applicant: Iwamatsu, Akihiro
 Applicant: Yoshikawa, Makiko
 Applicant: Yamada, Naoto
 Title of Invention: GLUCAN ELICITOR RECEPTOR, DNA MOLECULE TRANSFORMED WITH CODING THEREFOR, FUNGUS-RESISTANT PLANTS TRANSFORMED WITH THE DNA MOLECULE AND METHOD FOR CREATING THE PLANTS

Number of Sequences: 36

Correspondence Address:
 Addressee: Foley & Lardner
 Street: 3000 K Street, N.W., Suite 500
 City: Washington
 State: D.C.
 Country: USA
 Zip: 20007-5109

Computer Readable Form:
 Medium Type: Floppy disk
 Computer: IBM PC compatible
 Operating System: PC-Dos/MS-Dos

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 40.7387 Seconds
(without alignments)
2705.971 Million cell updates/sec

Title: US-10-088-666-21
Perfect score: 21
Sequence: 1 ccaagttaacaacgttgtt 21

Scoring table: IDENTITY_NTC
Gappp 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21sep04:**

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3: geneseqn2000s:**
4: geneseqn201as:**
5: geneseqn2001bs:**
6: geneseqn2002as:**
7: geneseqn2003bs:**
8: geneseqn2003as:**
9: geneseqn2003bs:**
10: geneseqn2003as:**
11: geneseqn2003bs:**
12: geneseqn2004as:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	21	100.0	21 5	AAF61586
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3	18	85.7	2215 3	AAC43884 C. vicina
4	17.8	84.8	207 8	ABX39064
5	17.8	84.8	211 8	ABX36896
6	17.8	84.8	229 8	ABX39055
7	17.8	84.8	239 8	ABX42886
8	17.8	84.8	242 8	ABX37833
9	17.8	84.8	247 8	ABX3018
10	17.8	84.8	292 8	ABX42572
11	17.8	84.8	301 8	ABX34921
12	17.8	84.8	308 8	ABX45227
13	17.8	84.8	340 8	ABX31596
14	17.8	84.8	341 8	ABX37025
15	17.8	84.8	342 8	ABX46317
16	17.8	84.8	348 8	ABX42328
17	17.8	84.8	350 8	ABX43307
18	17.8	84.8	360 8	ABX36914
19	17.8	84.8	360 8	ABX41692
20	17.8	84.8	366 8	ABX43494
21	17.8	84.8	366 8	ABX48929

ALIGNMENTS

RESULT 1
ID AAF61586
XX AAF61586 standard; DNA; 21 BP.
AC AAF61586;
XX DT 02-JUL-2001 (first entry)
DE Lactobacillus brevis 23S rRNA/5S rRNA specific DNA probe.
XX KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.
XX OS Lactobacillus brevis.
XX PN DE19945964-A1.
XX PD 05-APR-2001.
XX PF 24-SEP-1999; 99DE-01045964.
XX PR 24-SEP-1999; 99DE-01045964.
XX PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.
XX PI Fandke M., Gasch A., Berghoff K.;
XX DR WPI; 2001-246136/26.
XX PT Detecting contaminating microorganisms in brewing by nucleic acid amplification and hybridization, either non-specific or genus- or species specific.
XX Claim 9(1); Page 15; 48pp; German.
XX This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes specifically with a sequence common to all (A) or specific for one or more families, genera or species, and any formation of hybrids is detected. The method is used to detect, identify and/or characterize microorganisms in beer or brewing materials, particularly for detecting contamination. The method may detect the entire range of contaminating

CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 XX for high throughput analysis.

SQ Sequence 21 BP; 7 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 5; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.3; X%
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGGCAAAACGGTGT 21
 DB 1 CCAAGGCAAAACGGTGT 21

RESULT 2
 AA61566 standard; DNA; 267 BP.

XX AAF61566;
 XX DT 02-UTL-2001 (first entry)

XX Lactobacillus brevis 23S rRNA-spacer-5S rRNA DNA fragment.

XX 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

OS Lactobacillus brevis.
 XX PN DE1945964-AL.

XX PD 05-APR-2001.

XX PR 24-SEP-1999; 99DE-01045964.

XX PR 24-SEP-1999; 99DE-01045964.

XX PA (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX PI Fandke M, Gasch A, Berghof K;

XX DR WPI; 2001-246136/26.

XX PT Detecting contaminating microorganisms in brewing by nucleic acid

PT amplification and hybridization, either non-specific or genus- or species

PT -specific.

PS Claim 9(1); Page 9; 48pp; German.

XX This invention describes a novel method for detecting microorganisms (A)

CC of importance in brewing which comprises treating a sample with at least

CC two primers (P1) that hybridize to a consensus region in the nucleic acid

CC of (A), at least part of the microbial nucleic acid is amplified, the

CC amplicon is treated with at least one probe (P2) that hybridizes

CC specifically with a sequence common to all (A) or specific for one or

CC more families, genera or species, and any formation of hybrids is

CC detected. The method is used to detect, identify and/or characterize

CC microorganisms in beer or brewing material. Particularly for detecting

CC contamination. The method may detect the entire range of contaminating

CC microbes, either as a general test for contamination or as a test

CC specific for particular genera or (sub)species. It is quicker than known

CC microbiological methods, and can detect several organisms in the same

CC sample, including organisms not presently recognized as contaminants. The

CC method provides an early indication of contamination and can be automated

CC for high throughput analysis.

SQ Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 5; Length 267;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCAAGTCAACAGGTGT 21
 DB 103 CCAAGTCAACAGGTGT 123

RESULT 3

AZ43884/c
 ID AZ43884 standard; cDNA; 2215 BP.

AC AZ43884;

XX DT 10-MAR-2000 (first entry)

XX DE C. vicina LSP-2 cDNA.

XX KW Arylphorin; caliphorin; ABP; receptor-binding domain; plant protection;

XX KW hygiene; veterinary medicine; LSP-2; ds.

XX OS Caliphora vicina.

XX PN DE19824492-A1.

XX PD 09-DEC-1999.

XX PR 02-JUN-1998; 98DE-01024492.

XX PR 02-JUN-1998; 98DE-01024492.

XX PA (FARB) BAYER AG.

XX PT Scheller K, Hansen I, Gutmann V, Turberg A;

XX DR WPI; 2000-05431/05.

XX DR P-PSDB; ARX1007.

XX PT Receptor-binding domain useful for identifying new substances for plant

XX protection, hygiene or veterinary medicine.

XX RS Example A; Page 40-43; 50pp; German.

XX This invention describes novel receptor-binding domain of the Calliphora vicina arylphorin protein (also known as calliphorin). The receptor-

CC binding domain, nucleic acid constructs, host cells and antibodies described in the invention are useful for discovering new active

CC substances for plant protection, hygiene or veterinary medicine, in

CC particular for combination, which influences the interaction between

CC arylphorins and the arylphorin receptor. This sequence encodes the C. vicina LSP-2 protein.

XX SQ Sequence 2215 BP; 634 A; 524 C; 433 G; 524 T; 0 U; 0 Other;

XX Query Match 85.7%; Score 18; DB 3; Length 2215;

XX Best Local Similarity 100.0%; Pred. No. 72; X%

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 CCAAGTCAACAGGTGT 18
 XX DB 1687 CCAAGTCAACAGGTGT 1670

RESULT 4

ABX39064
 ID ABX39064 standard; cDNA; 207 BP.

XX AC ABX39064;

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GenCore version 5.1.6

Om nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:05:13 ; Search time 4454.01 Seconds

(without alignments) 284.416 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: tatatggaaatggacccct.....agtagttggggatcgcccc 267

Scoring table: IDENTITY_NUC

GapOp 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1819865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Result No.	Score	Query	Match	Length	DB	ID	Description
1	163.4	EST:*	gb_est1:*	61.2	793	8	B2369094
2	105.4	EST:*	gb_est2:*	39.5	3268	8	BH770509
3	9.5	gb_hnc:*	gb_est3:*	39.5	6499	8	BH771024
4	4.2	gb_est3:*	gb_est4:*	21.8	342	7	CR469421
5	56.4	gb_est4:*	gb_est5:*	21.1	690	8	BH687637
6	51.6	gb_est5:*	gb_est6:*	19.3	277	7	CR477397
7	50.4	gb_est6:*	gb_gss2:*	18.9	1258	8	BH770557
8	50.2	gb_gss2:*	gb_gss2:*	18.8	391	8	AQ990586
9	50.2	gb_gss2:*	gb_gss2:*	18.8	607	8	AQ998492
10	49.2	gb_gss2:*	gb_gss2:*	18.4	393	8	CC14308
11	49.2	gb_gss2:*	gb_gss2:*	18.4	453	5	BUD003208
12	48.6	gb_gss2:*	gb_gss2:*	18.2	833	9	CL659016
13	48.6	gb_gss2:*	gb_gss2:*	18.2	844	9	CL664279
14	48.6	gb_gss2:*	gb_gss2:*	18.2	872	9	CL662374
15	48.6	gb_gss2:*	gb_gss2:*	18.2	879	9	CL667131
16	47.2	gb_gss2:*	gb_gss2:*	17.7	255	8	BH770635
17	47.2	gb_gss2:*	gb_gss2:*	17.7	333	7	CR470260
18	47.2	gb_gss2:*	gb_gss2:*	17.6	698	9	AG613316
19	46	gb_gss2:*	gb_gss2:*	17.2	534	9	CL681720
20	45	gb_gss2:*	gb_gss2:*	17.2	664	9	AG61279
21	46	gb_gss2:*	gb_gss2:*	17.2	735	9	CL667389
22	45.8	gb_gss2:*	gb_gss2:*	17.2	544	8	AQ998631
23	45.8	gb_gss2:*	gb_gss2:*	17.2	655	8	AQ990982
24	44.8	gb_gss2:*	gb_gss2:*	16.8	1073	8	AQ99631

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

B2369094

LOCUS BZ369094

DEFINITION Cot100.1-2.D04 Maize Cot100 library

survey sequence.

ACCESSION BZ369094

VERSION BZ369094.1

GI:25122715

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

SPERMATOPHYTA; VIRIDILYMPHTAE; STREPTOPHYTA; EMBRYOPHYTA; Liliopsida; Poales; Poaceae; PACCDAD

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; clade; Pandidae; Andropogoneae; Zea.

1 (bases 1 to 793)

REFERENCE Yuan,Y., Samiguel,P., and Bennetzen,J.L.

AUTHORS High Cot sequence analysis of the maize genome

TITLE Unpublished (2003)

JOURNAL Contact: Bennetzen JL

COMMENT Department of Biological Sciences

Purdue University

Hansen 339#, Purdue University, West Lafayette, IN 47907, USA

Tel: 765 494 4919

Fax: 765 496 1496

Email: maize@ilbo.bio.purdue.edu

Forward and reverse reads were assembled when significant overlap was detected.

Seq primer: T7 and T3

FEATURES source

Class: shotgun

Location/Qualifiers I..793

FEATURES source

Class: shotgun

Location/Qualifiers I..793

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

/db_xref="taxon:4577"

/dev_stage="10 days seedling"

/lab_host="DH10B"

/clone_lab="Maize Cot100 library"

/note="Organ: young leaves; Vector: pcr4TOPO; Maize genomic DNA was Sheared to fragments averaging about 1.8 kb, was denatured and then reassociated in T-X SSC at 65°C. After a given Cot value was reached, aliquots were run over a hydroxypapitate (HAP) column in order to separate single stranded DNA from double stranded DNA. The single stranded DNA was then converted to a double stranded form with one round of Klenow DNA polymerase treatment with random 9-mer primers. The double-stranded fragments were then further size-selected over an agarose

gel and cloned into the PCR4 TOPO vector."

ORIGIN

Query Match Similarity 61.2%; Score 163.4; DB 8; Length 793;
Best Local Similarity 81.1%; Pred. No. 1.3e-40; Mismatches 0; Indels 4; Gaps 2;
Matches 215; Conservative 0; Mismatches 46; Indels 4; Gaps 2;

Qy 3 TATGGAGTGTAGACCCCTGAGAGATGAGGAGATGGCGAATAGCAGCGCGTG 62
Db 132 TTGGAGTGTAGACCCCACTAGAGATGAGTGTGGTAGATGAGTGAAGTGGTG 191
Qy 63 AGGCCTGGAGGACAGACTAACTCGCTGAGGACTTAACAGTCACAGTGTG 122
Db 192 ACGCATGGACGGCACATTACTATCGCTGAGGACTTAACAGTCACAGTGTG 251
Qy 123 TTTCGAGATAATTGATATCTAGTTGAGGAAGTCTTATAGTGGTG 182
Db 252 CTTGATG-T-GAAAGATATGTTAGTTGAAAGCAAG---CTTCAAGTGGGTG 307
Qy 183 GCGTAGCTGAGGATACCTTCCATGCCAGAACACAGAGTAAAGCTTCAACAC 242
Db 308 ATGATGCCAGAAGATACCTTCCATGCCAGAACACAGAGTAAAGCTTCAACAC 367
Qy 243 CCGATAGTACTGGGGATGCCCC 267
Db 368 CCAAAGTGTGGGATGCCCC 392

RESULT 2

LOCUS BH70998 3268 bp DNA Linear GSS 01-MAY-2002
DEFINITION LMGt7g721 MG1363 Random Sequence Tag Library Lactococcus lactis
ACCESSION BH70998
VERSION BH70998.1 GI:20373955
JOURNAL GSS.
ORGANISM Lactococcus lactis subsp. cremoris
KEYWORDS Lactococcus; Firmicutes; Lactobacillales; Streptococcaceae;
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
COMMENT INRA
INRA INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokin@jouy.inra.fr
Contact: Sorokin A
Genetique Microbienne

REFERENCE 1 (bases 1 to 3268)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
KEYWORD Sci. Aliments (2002) In press
JOURNAL Contact: Sorokin A
COMMENT INRA
INRA INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokin@jouy.inra.fr
best homologue in strain IIL403 is YWGA (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
Location/Qualifiers

FEATURES source

1. .3268 /organism="Lactococcus lactis subsp. cremoris"
/mol_type="Genomic DNA"
/strain="MG1363"
/sub_species="cremoris"
/db_xref=taxon:1359
/clone_lib="MG1363 Random Sequence Tag Library"
/note="vector: pSGM2; Site 1: SmaI; Library of
chromosomal fragments of L.lactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
/origin

Query Match Similarity 39.5%; Score 105.4; DB 8; Length 6499;
Best Local Similarity 67.3%; Pred. No. 5.3e-22; Mismatches 0; Indels 14; Gaps 2;
Matches 185; Conservative 0; Mismatches 76; Indels 14; Gaps 2;

Qy 7 GAAGTGTAGACCCCTGAGAGATGAGTGTGGAGTAGGAGCGGCCGIGAGC 66
Db 5177 GAATGAGTACGACGAGATGATCTGGTAGATGAGTGGCTGAGATGCGAGAC 5236
Qy 67 GTGGAGCGGACGACTAACTCGCTGAGGACTTAACAA-----GTCAACAC 115
Db 5237 TTGGAGCGGACGACTAACTCGCTGAGGACTTAACAA-----GTCAACAC 5296
Qy 116 GTAGTGTGAGGAGATGAGTGGGAGGAGTGGCTGAGAGTGTCTCTATAG 420

ORIGIN

Query Match Similarity 39.5%; Score 105.4; DB 8; Length 6499;
Best Local Similarity 67.3%; Pred. No. 4.6e-22; Mismatches 0; Indels 14; Gaps 2;
Matches 185; Conservative 0; Mismatches 76; Indels 14; Gaps 2;
/origin

Query Match Similarity 39.5%; Score 105.4; DB 8; Length 3268;
Best Local Similarity 67.3%; Pred. No. 4.6e-22; Mismatches 0; Indels 14; Gaps 2;
Matches 185; Conservative 0; Mismatches 76; Indels 14; Gaps 2;
7 GAAGTGTAGACCCCTGAGAGATGAGTGTGGAGTAGGAGCGGCCGIGAGC 66
Qy 67 GTGGAGCGGACGACTAACTCGCTGAGGACTTAACAA-----GTCAACAC 115
Db 5237 TTGGAGCGGACGACTAACTCGCTGAGGACTTAACAA-----GTCAACAC 5296
Qy 116 GTAGTGTGAGGAGATGAGTGGGAGGAGTGGCTGAGAGTGTCTCTATAG 175

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Om nucleic - nucleic search, using sw model

Run on: November 15, 2004, 11:50:19 ; Search time 461.036 Seconds
(Without alignments)
3127.976 Million cell updates/sec

Title: US-10-088-666-1
Perfect score: 267
Sequence: 1 tatatggaaatggaccct.....agtagttggggatcgccc 267

Scoring table: IDENTITY.NUC
Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 270493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

- Published Applications NA:*
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- 2: /cgna_6/prodata/2/pbpna/pct_new_pub.seq:*
- 3: /cgna_6/prodata/2/pbpna/us06_pubcomb.seq:*
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- 18: /cgna_6/prodata/2/pbpna/us10_new_pub.seq:*
- 19: /cgna_6/prodata/2/pbpna/us11_new_pub.seq:*
- 20: /cgna_6/prodata/2/pbpna/us00_new_pub.seq:*
- 21: /cgna_6/prodata/2/pbpna/us60_pubcomb.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	115.8	43.4	31702	16	US-10-398-221-3 Sequence 3, Appl1
C 2	115.6	43.3	3510	8	US-08-961-527-53 Sequence 53, Appl1
C 3	115.6	43.3	3510	16	US-10-158-844-53 Sequence 53, Appl1
C 4	115.6	43.3	3989	9	US-09-070-922A-359 Sequence 359, Appl1
C 5	115.6	43.3	5048	10	US-03-884-465A-2 Sequence 2, Appl1
C 6	115.6	43.3	8411	8	US-08-961-527-16 Sequence 16, Appl1
C 7	115.6	43.3	8411	16	US-08-158-844-16 Sequence 16, Appl1
C 8	115.6	43.3	11915	8	US-08-961-527-96 Sequence 96, Appl1
C 9	115.6	43.3	11915	16	US-10-158-844-96 Sequence 96, Appl1
C 10	114.2	42.8	1389	16	US-10-398-221-3318 Sequence 3318, Appl1
C 11	114.2	42.8	2631	16	US-10-398-221-2 Sequence 2, Appl1
C 12	114.2	42.8	5349	16	US-10-398-221-3795 Sequence 3795, Appl1

ALIGNMENTS

RESULT 1
US-10-398-221-3/C
Sequence 3, Application US/10398221
Sequence No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KUNSI, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 34A 702 - US CURRENT APPLICATION NUMBER: US/10/398-221
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
PRIOR FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: FR 00/012 697
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 4025
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 31702
TYPE: DNA
ORGANISM: Listeria innocua
US-10-398-221-3

Query Match Best Local Similarity 43.4%; Score 115.8; DB 16; Length 31702; Matches 189; Conservative 0; Mismatches 72; Indels 10; Gaps 2;

QY 6 GGAGTTGAGCCCTGAGAGATCGGTAGATGGCTGGAGAGGAGGCCGCGAGG 65
D 30605 GAAAGTAAAGATCCTGAAGATGATCAGTAGATGGTTGGAGTGCGAGTGGATATA 30547
QY 66 CGTGGAGGGACCACTAATCGTCAGGACTAACAGTCACACGATGTT 125
D 30546 CATGGAGGGACAATTAATCGTCAGGACTAACAGTCACACGATGTT-TAC 30488

QY 126 CGAGAATATGAAATACTAGTTGGGAGAACCTCT-----CTTATAGT 176
;
Db 30487 CTAACGAACTTCTTCCTCTAGTTGGAGAGCAACTTCAACACTGCATATGT 30428
;
QY 177 GTGGTGGCATAGCTGAAGATACAGTACCTGTCATGCCATGCCAGACAGAGTTAGCTC 236
;
Db 30427 CTGGTAGTTTGGCGAAAGTGACCCCTCCATCCGAACRGSTGTRAGCTC 30368
;
Db 30367 TCTGCCCAATGGTAGTGGGGCTCCCC 30337

RESULT 2
US-08-961-527-53/C
; Sequence 53, Application US/0891527
; Publication No. US2002003223A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE: 1996-10-31
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 36,373
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PEP340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 3510 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear
US-08-961-527-53

Query Match 43.3%; Score 115.6; DB 8; Length 3510;
Best Local Similarity 66.8%; Pred. No. 1.1e-26; Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;
Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;

QY 1 TATATCGAGTAGACCCCTGAGAGATAGCTGGTAGATGGCTGAGAGCAGCGCG 60
;
Db 3288 TATATCGAGTAGACCCCTGAGAGATAGCTGGTAGATGGCTGAGAGCAGCGCG 3229
;
QY 61 TGAGGCTGGCGGACGACTAATGGTAGGACTAACAGTCACAACGAGT 120
;
Db 3228 CGACACATGCTGGACTAATCTAATAGCTGAGGACTTATCCAAAGTACTGAGATA 3169
;
QY 121 TGTTCGAGAATATGAAATACTAGTTGGAGAAG-----TTCTAT 173
;
Db 3168 TGAAGCGAACGGTTCTTAATGATAGATATTCATTGTAGTTACTCAG 3109
;
QY 174 AGTGTGGCGATAGCTGAAGAACCTGTCATCCGAAACAGAGTAACT 233
;
Db 3108 AGTAACTGACGATAGCTGAGGATACACTGTACCTGAGAGTAACT 3049
;
QY 174 AGTGTGGCGATAGCTGAAGAACCTGTCATCCGAAACAGAGTAACT 233
;
Db 3048 CCTGAGCGCCGAAAGTGGGGTGGCCC 3015

RESULT 3
US-10-158-944-53/C
; Sequence 53, Application US/10158844
; Publication No. US2004029118A1
; GENERAL INFORMATION:
; APPLICANT: Kunsch et al.
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: Dell Latitude Pentium 3
OPERATING SYSTEM: Windows 98
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/10/158, 844
FILED DATE: 03-Jun-2002
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
FILED DATE: 1997-10-30
APPLICATION NUMBER: US 60/0029, 960
FILED DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PEP340P1D1
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 3510 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-158-844-53

Query Match 43.3%; Score 115.6; DB 16; Length 3510;
Best Local Similarity 66.8%; Pred. No. 1.1e-26; Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;
Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;

QY 1 TATATCGAGTAGACCCCTGAGAGATAGCTGGTAGATGGCTGAGAGCAGCGCG 60
;
Db 3288 TATATCGAGTAGACCCCTGAGAGATAGCTGGTAGATGGCTGAGAGCAGCGCG 3229
;
QY 61 TGAGGCTGGCGGACGACTAATGGTAGGACTAACAGTCACAACGAGT 120
;
Db 3228 CGACACATGCTGGACTAATCTAATAGCTGAGGACTTATCCAAAGTACTGAGATA 3169
;
QY 121 TGTTCGAGAATATGAAATACTAGTTGGAGAAG-----TTCTAT 173
;
Db 3168 TGAAGCGAACGGTTCTTAATGATAGATATTCATTGTAGTTACTCAG 3109
;
QY 174 AGTGTGGCGATAGCTGAAGAACCTGTCATCCGAAACAGAGTAACT 233
;
Db 3108 AGTAACTGACGATAGCTGAGGATACACTGTACCTGAGAGTAACT 3049
;
QY 174 AGTGTGGCGATAGCTGAAGAACCTGTCATCCGAAACAGAGTAACT 233
;
Db 3048 CCTGAGCGCCGAAAGTGGGGTGGCCC 3015

Copyright (c) 1993 - 2004 Compugen Ltd.	GenCore version 5.1.6	c 28	104.4	39.1	386	4	US-08-956-171E-4054	Sequence 4064, AP
OM nucleic - nucleic search, using sw model		c 29	39.1	386	4	US-08-956-171E-3114	Sequence 4064, AP	
Run on:	November 15, 2004, 11:05:14 ; Search time 115.459 Seconds	c 30	101.2	37.9	6591	4	US-08-956-171E-3114	Sequence 3114, AP
Title:	(without alignments)	c 31	101.2	37.9	6591	4	US-08-956-171E-3114	Sequence 3114, AP
Perfect score:	267	c 32	100.8	37.8	400	4	US-08-956-171E-3168	Sequence 3768, AP
Sequence:	1 tatatggaaatggacccct.....agtagttggggatcgcccc 267	c 33	100.8	37.8	400	4	US-08-956-171E-3168	Sequence 3768, AP
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Searched:	824507 sqs, 35539441 residues	c 36	100.6	37.7	400	4	US-08-956-171E-3638	Sequence 3638, AP
Total number of hits satisfying chosen parameters:		c 37	100.6	37.7	400	4	US-08-956-171E-3748	Sequence 3748, AP
Minimum DB seq length: 0		c 38	100.6	37.7	458	4	US-08-956-171E-3757	Sequence 3757, AP
Maximum DB seq length: 2000000000		c 39	100.6	37.7	458	4	US-08-956-171E-3757	Sequence 3757, AP
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	3: /cgm2_6/ptodata/l/ina/61-COMB.seq:*	c 43	100.6	37.7	30246	4	US-08-956-171E-56	Sequence 56, AP
	4: /cgm2_6/ptodata/l/ina/6B-COMB.seq:*	c 44	100.4	37.6	400	4	US-08-956-171E-3611	Sequence 3611, AP
	5: /cgm2_6/ptodata/l/ina/backfiles1.seq:*	c 45	100.4	37.6	400	4	US-08-956-171E-3634	Sequence 3634, AP
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		ALIGNMENTS						
SUMMARIES								
Result No.	Score	Query Length	DB ID	Description				
c 1	115.6	43.3	3510	4 US-08-956-1527-53	RESULT 1 US-08-951-527-53/C Sequence 53, Application US/08961527 Patent No. 6420135			
c 2	115.6	43.3	8411	4 US-08-961-527-53	GENERAL INFORMATION: APPLICANT: Charles Kunsch TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391			
c 3	115.6	43.3	11915	4 US-08-961-527-96	CORRESPONDENCE ADDRESS: ADDRESSEE: Human Genome Sciences, Inc.			
c 4	111.8	41.9	2725	4 US-09-710-279-3512	STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA			
c 5	111.8	41.9	2879	4 US-09-710-279-4402	ZIP: 20850			
c 6	111.8	41.9	3012	4 US-09-710-279-707	CURRENT APPLICATION DATA: COMPUTER READABLE FORM: OPERATING SYSTEM: MSDOS version 6.2 SOFTWARE: ASCII TEXT			
c 7	111.8	41.9	3019	4 US-09-710-279-918	APPLICATION NUMBER: US/08/961,527			
c 8	111.8	41.9	3232	4 US-09-710-279-916	FILING DATE: CLASSIFICATION: 424 PRIORITY APPLICATION DATA: APPLICATION NUMBER:			
c 9	111.8	41.9	3305	4 US-09-710-279-4156	ATTORNEY/AGENT INFORMATION: NAME: Brookes,A. Anders REGISTRATION NUMBER: 36,373 REFERENCE DOCKET NUMBER: P3340PL			
c 10	111.8	41.9	3342	4 US-09-710-279-4283	TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8512 TELEFAX: (301) 309-8512			
c 11	111.8	41.9	3405	4 US-09-710-279-3903	INFORMATION FOR SEQ ID NO: 53: SEQUENCE CHARACTERISTICS: LENGTH: 3510 base pairs			
c 12	111.8	41.9	3608	4 US-09-710-279-3759	TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear			
c 13	111.8	41.9	3625	4 US-09-710-279-3658	US-08-961-527-53			
c 14	111.8	41.9	3656	4 US-09-710-279-3739	Query Match Best Local Similarity 66.8%; Pred. No. 8e-32; Matches 183; Conservative 0; Mismatches 84; Indels 7; Gap 1;			
c 15	111.8	41.9	3845	4 US-09-710-279-3520	QY 1 TATATGGAGTAGACGCCCTGAGAGATGATGGATAGCTGAAAGTCACCGCG 60			
c 16	111.8	41.9	4106	4 US-09-710-279-3684	Sequence 3624, AP			
c 17	111.6	41.8	4106	4 US-08-956-171E-508	Sequence 3624, AP			
c 18	111.6	41.8	840	4 US-08-978-1986A-3738	Sequence 3624, AP			
c 19	110.2	41.3	1089	4 US-09-710-279-4334	Sequence 3624, AP			
c 20	110.2	41.3	3012	4 US-09-710-279-3683	Sequence 3624, AP			
c 21	110.2	41.3	3030	4 US-09-710-279-3916	Sequence 3624, AP			
c 22	110.2	41.3	3937	4 US-09-710-279-3772	Sequence 3624, AP			
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c 24	109.6	40.0	400	4 US-08-781-986A-3738	Sequence 3624, AP			
c 25	108.6	40.7	2662	4 US-09-710-279-4334	Sequence 3624, AP			
c 26	39.7	400	4 US-08-956-171E-3624	Sequence 3624, AP				
c 27	39.7	400	4 US-08-781-986A-3624	Sequence 3624, AP				

RESULT 2
US-08-961-527-16
; Sequence 16, Application US/08961527
; Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11915 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-961-527-16

Query Match 43.3%; Score 115.6; DB 4; Length 8411;
Best Local Similarity 66.8%; Pred. No. 1.3e-31;
Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;

QY 1 TATATGGAAAGTAAACCCCTGAGAGATGATCGAGTAGATGGCTGGAGTAGCAGGCCCG 60
Db 316 TATATATCGTAAGGCCCTGAGAGATGATCGAGTAGATGGCTGGAGTAGCAGGCCCG 375

QY 61 TGAGCCGTGGAGGCCGACTATCGTGAGGACTAACGAGTTACCAAGTCACAGCTAGT 120
Db 376 CGACACATGTAGCCGACTAATCATCTCGAGACTTACAGTAATGAGATA 435

QY 121 TGTTCGAGATAATGATAATCTAGTTGAGGAGAG-----TCTCTAT 173

Db 3108 AGTAACTGACGATAGCTAGGATAGATCAATTGAGTTAGATTACCTGACAGATTAAC 3049

RESULT 3
US-08-961-527-96
; Sequence 96, Application US/08961527
; Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 11915 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-961-527-96

Query Match 43.3%; Score 115.6; DB 4; Length 11915;
Best Local Similarity 66.8%; Pred. No. 1.6e-31;
Matches 183; Conservative 0; Mismatches 84; Indels 7; Gaps 1;

QY 1 TATATGGAAAGTAAACCCCTGAGAGATGATCGAGTAGATGGCTGGAGTAGCAGGCCCG 60
Db 255 TATATATCGTAAGGCCCTGAGAGATGATCGAGTAGATGGCTGGAGTAGCAGGCCCG 314

QY 61 TGAGCCGTGGAGGCCGACTATCGTGAGGACTAACGAGTTACCAAGTCACAGCTAGT 120
Db 315 CGACACATGTAGCCGACTAATCATCTCGAGACTTACAGTAATGAGATA 435

QY 121 TGTTCGAGATAATGATAATCTAGTTGAGGAGAG-----TCTCTAT 173

Db 375 TCAAGCGACGCTTCTAACTGATAATGAGATCAATTGAGTAGATTACCTGACAGATTAAC 434

QY 174 AGTGTGTGAGGATGCTGGAGTACACTGTGTCAGTACGAGTAACGAGTTACCTGACAGATTAAC 233

Db 556 CCTAGACGCCGAGTAGTGAGGTGGTGCCTCC 589

Db 234 TTGAGACGCCGATGAGTAGGGATGCCCTACCTTACCCATGCCAACAGAGATTAAC 233

Db 314 TGTTCGAGATAATGATAATCTAGTTGAGGAGAG-----TCTCTAT 173

Db 496 AGTAACTGACGATAGCTAGGATAGATCAATTGAGTTAGATTACCTGACAGATTAAC 555

Db 3228 CGACACATGTAGCCGACTAATCATCTCGAGACTTACAGTAATGAGATA 3169

QY 171 TGTTCGAGATAATGATAATCTAGTTGAGGAGAG-----TCTCTAT 173

Db 3168 TGAAGCGACCGTTCTTAATTGATAGATCAATTGAGTTAGATTACCTGACAGATTAAC 3049

QY 234 TTGAGACGCCGATGAGTAGGGATGCCCTACCTTACCCATGCCAACAGAGATTAAC 434

Db 3048 CCTAGACGCCGAGTAGTGAGGTGGTGCCTCC 589

QY 3015 CCTAGACGCCGAGTAGTGAGGTGGTGCCTCC 3015

Db 436 TGAAGCGACGCCGACTATCGTGAGGAGTACACGCTGAGTACAGTAAAG 495

Db 174 AGTGTGTGAGGATGCTGGAGTACACTGTGTCAGTACGAGTAACGAGTTACCTGACAGATTAAC 233

Db 496 AGTAACTGACGATAGCTAGGATAGATCAATTGAGTTAGATTACCTGACAGATTAAC 555

Db 314 TGTTCGAGATAATGATAATCTAGTTGAGGAGAG-----TCTCTAT 173

Db 435 AGTAACTGACGATAGCTAGGATAGATCAATTGAGTTAGATTACCTGACAGATTAAC 494

CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

SQ Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

Query Match 100.0%; Score 267; DB 5; Length 267;
 Best Local Similarity 100.0%; Pred. No. 4.e-83;
 Matches 267; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ Sequence 267 BP; 77 A; 51 C; 77 G; 62 T; 0 U; 0 Other;

QY 1 TATATGGAATTAAGACCCCTGAGAATGACAGGATAGGGTGGAGTAGCAGCGCG 60
 Db 1 TATATGGAATTAAGACCCCTGAGAATGACAGGATAGGGTGGAGTAGCAGCGCG 60
 QY 61 TGAGGCTGGAGGCCAACACTATCTGCTGAGGACTTACCAAGTCACAGTGT 120
 Db 61 TGAGGCTGGAGGCCAACACTATCTGCTGAGGACTTACCAAGTCACAGTGT 120
 QY 121 TGTTCAGAAATAATGAAATACTAGTTGGGGAGAGTCCTATAGTGCG 180
 Db 121 TGTTCAGAAATAATGAAATACTAGTTGGGGAGAGTCCTATAGTGCG 180
 QY 181 TGGCGATAGCCGAGGATAACCTTCATGGGAAACAGAGTTAGCTCAGA 240
 Db 181 TGGCGATAGCCGAGGATAACCTTCATGGGAAACAGAGTTAGCTCAGA 240
 QY 241 CGCGATAGTGGTGGGGAGGCC 267
 Db 241 CGCGATAGTGGTGGGGAGGCC 267

RESULT 2

AAF61572
 ID AAF61572 standard; DNA; 317 BP.

XX AAF61572;
 XX AC ;
 XX DT 02-JUL-2001 (first entry)

XX DR L. coryniformis ssp torquens 23S rRNA-spacer-5S rRNA DNA fragment.
 XX KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

XX OS lactobacillus coryniformis.
 XX PN DE19945964-A1.

XX PR 05-APR-2001.

XX PP 24-SEP-1999; 99DE-01045964.

XX PR 24-SEP-1999; 99DE-01045964.

XX PR (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX PT Detecting contaminating microorganisms in brewing, by nucleic acid
 XX PT amplification and hybridization, either non-specific or genus- or species
 XX PT -specific.

PS Claim 9(i); Page 10; 48pp; German.

This invention describes a novel method for detecting microorganisms (A) of importance in brewing which comprises treating a sample with at least two primers (P1) that hybridize to a consensus region in the nucleic acid of (A), at least part of the microbial nucleic acid is amplified, the amplicon is treated with at least one probe (P2) that hybridizes

CC specifically with a sequence common to all (A) or specific for one or
 CC more families, genera or species, and any formation of hybrids is
 CC detected. The method is used to detect, identify and/or characterize
 CC microorganisms in beer or brewing materials, particularly for detecting
 CC contamination. The method may detect the entire range of contaminating
 CC microbes, either as a general test for contamination or as a test
 CC specific for particular genera or (sub)species. It is quicker than known
 CC microbiological methods, and can detect several organisms in the same
 CC sample, including organisms not presently recognized as contaminants. The
 CC method provides an early indication of contamination and can be automated
 CC for high throughput analysis

SQ Sequence 317 BP; 90 A; 59 C; 96 G; 72 T; 0 U; 0 Other;

Query Match 58.6%; Score 156.4; DB 5; Length 317;
 Best Local Similarity 78.3%; Pred. No. 3.1e-44;
 Matches 216; Conservative 0; Mismatches 51; Indels 9; Gaps 2;

SQ Sequence 317 BP; 90 A; 59 C; 96 G; 72 T; 0 U; 0 Other;

QY 1 TATATGGAATTAAGACCCCTGAGAATGACAGGATAGGGTGGAGTAGCAGCGCG 60
 Db 24 TATATGGAATTAAGACCCCTGAGAATGACAGGATAGGGTGGAGTAGCAGCGCG 60
 QY 61 TGAGGCTGGAGGCCAACACTATCTGCTGAGGACTTACCAAGTCACAGTGT 120
 Db 84 TGAGGCTGGAGGCCAACACTATCTGCTGAGGACTTACCAAGTCACAGTGT 120
 QY 116 GAGTGTCTTCGAGAAATACTAGTTGGGGAGAGTCCT 171
 Db 144 GAGTGTCTTCGAGAAATACTAGTTGGGGAGAGTCCT 171
 QY 172 ATAGTGGTGGGGATAGCTGGAGGATACCTGTCCATGCGAACACAGAGTAA 231
 Db 204 GAGTGTCTTCGAGAAATACTAGTTGGGGAGAGTCCT 263
 QY 232 GCTTCACACGGCATGTTGGGGATGGCCC 267
 Db 264 GCTTCACACGGCATGTTGGGGAGAGTCCT 299

RESULT 3

AAF61571
 ID AAF61571 standard; DNA; 317 BP.

XX AAF61571;
 XX AC ;
 XX DT 02-JUL-2001 (first entry)

XX DR L. coryniformis ssp coryniformis 23S rRNA-spacer-5S rRNA DNA fragment.
 XX KW 23S rRNA; 5S rRNA; detection; probe; brewing; beer; contamination; ss.

XX OS lactobacillus coryniformis.
 XX PN DE19945964-A1.

XX PR 05-APR-2001.

XX PP 24-SEP-1999; 99DE-01045964.

XX PR 24-SEP-1999; 99DE-01045964.

XX PR (BIOT-) BIOTECON DIAGNOSTICS GMBH.

XX PT Detecting contaminating microorganisms in brewing, by nucleic acid
 XX PT amplification and hybridization, either non-specific or genus- or species
 XX PT -specific.

PS Claim 9(i); Page 10; 48pp; German.

Detecting contaminating microorganisms in brewing, by nucleic acid
 PT amplification and hybridization, either non-specific or genus- or species
 PT -specific.

PS Claim 9(i); Page 10; 48pp; German.

Page 1

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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 12:43:29 ; Search time 2084.68 Seconds

(without alignments) 6056.719 Million cell updates/sec

Title: US-10-088-666-1

Perfect score: 267

Sequence: 1 tataatggaaatggacccct.....agtagttggatcgcccc 267

Scoring table: Oligo-Nuc_

Gapop 60.0 , Gapext 60.0

Searched: 4526729 seqs, 23644849745 residues

Wordsize: 11

Total number of hits satisfying chosen parameters: 1357868

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database	GenBank*	gb_bt:*	gb_btq:*	gb_inl:*	gb_inr:*	gb_itn:*	gb_itq:*	gb_lph:*	gb_lpi:*	gb_pcr:*	gb_pcr:*	gb_sts:*	gb_sy:*	gb_un:*	gb_vti:*	
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	8:															
	9:															
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	12:															
	13:															
	14:															

Pred: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
1	267	100.0	267	6	AX105729	AX105729 Sequence
2	92	34.5	117	1	LBRRNNS	X03026 Lactobacillus
3	73	27.3	326	6	AX105730	AX105730 Sequence
4	50	18.7	338	6	AX105733	AX105733 Sequence
5	50	18.7	351	6	AX105731	AX105731 Sequence
6	50	18.7	414	6	AX105732	AX105732 Sequence
7	50	18.7	1541	1	AF098107	Lactobacillus
8	44	16.5	249	6	AR397133	AR397133 Sequence
9	44	16.5	3989	6	BD193765	BD193765 Enterococcus
10	44	16.5	9797	6	BD193956	BD193956 Enterococcus
11	44	16.5	22960	6	BDD193751	BDD193751 Enterococcus
12	44	16.5	176545	1	AE016557	AE016557 Enterococcus
13	44	16.5	177911	1	AB012206	AB012206 Lactobacillus
14	44	16.5	183043	6	AX926713	AX926713 Sequence
15	44	16.5	300478	1	AE017201	AE017201 Lactobacillus
16	44	16.5	300886	1	AE017205	AE017205 Lactobacillus
17	44	16.5	301488	1	AB016550	AB016550 Enterococcus
18	44	16.5	304454	1	AE016556	AE016556 Enterococcus
19	44	16.5	326434	1	AE016947	AE016947 Enterococcus

REFERENCE	1 (bases 1 to 117)
AUTHORS	Woesz, C.R., Luehrsen, K.R., Pribula, C.D. and Fox, G.E.
TITLE	Sequence characterization of 5S ribosomal RNA from eight gram positive prokaryotes
JOURNAL	J. Mol. Evol. 8 (2), 143-153 (1976)
MEDIUM	7709046
PUBLISHED	823342
FEATURES	Location/Qualifiers 1. .117 /organism="Lactobacillus brevis" /mol-type="genomic DNA" /db_xref="taxon:1580"
source	/product="5S ribosomal RNA" 1. .117 /product="5S ribosomal RNA"
ORIGIN	Query Match 34.5%; Score 92; DB 1; Length 117; Best Local Similarity 100.0%; Pred. No. 4.6e-41; Mismatches 0; Indels 0; Gaps 0; . Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0; .
LOCUS	AX105730
DEFINITION	Sequence 2 from Patent WO0123605.
VERSION	AX105730.1 GI:13921743
KEYWORDS	QY 176 TGTGGCGGATAGCCATGCGTCCATGCCAACACAGATTAACTT 235 Db 1 TGTGGCGGATAGCCATGCCAACACAGATTAACTT 60
SOURCE	QY 236 CGCACCGGATAGTAGTGCGGGATGCC 267 Db 61 CGCACCGGATAGTAGTGCGGGATGCC 92
ORGANISM	Lactobacillus lindneri
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ORIGIN	Query Match 34.5%; Score 92; DB 1; Length 117; Best Local Similarity 100.0%; Pred. No. 4.6e-41; Mismatches 0; Indels 0; Gaps 0; . Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0; .
LOCUS	AX105730
DEFINITION	Sequence 2 from Patent WO0123605.
VERSION	AX105730.1 GI:13921743
KEYWORDS	QY 176 TGTGGCGGATAGCCATGCGTCCATGCCAACACAGATTAACTT 235 Db 1 TGTGGCGGATAGCCATGCCAACACAGATTAACTT 60
SOURCE	QY 236 CGCACCGGATAGTAGTGCGGGATGCC 267 Db 61 CGCACCGGATAGTAGTGCGGGATGCC 92
ORGANISM	Lactobacillus lindneri
FEATURES	Location/Qualifiers 1. .267 /organism="Lactobacillus brevis" /mol-type="unassigned DNA" /db_xref="taxon:1580"
ORIGIN	Query Match 27.3%; Score 73; DB 6; Length 326; Best Local Similarity 100.0%; Pred. No. 3.5e-30; Mismatches 0; Indels 0; Gaps 0; . Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0; .
LOCUS	AX105733
DEFINITION	Sequence 5 from Patent WO0123605.
VERSION	AX105733.1 GI:13921746
KEYWORDS	QY 172 ATATGTTGGGGATACCTGGAGGATACCCCTGTCCATGCCAACACAGAGTTA 231 Db 204 ATATGTTGGGGATACCTGGAGGATACCCCTGTCCATGCCAACACAGAGTTA 263
SOURCE	QY 232 GCTTCAGCAGGCC 244 Db 264 GCTTCAGCAGGCC 276
ORGANISM	Lactobacillus brevis
RESULT 2	LRRNNS LRRNNS 117 bp DNA linear BCT 06-JUN-2003
LOCUS	Lactobacillus brevis 5S ribosomal RNA.
DEFINITION	Lactobacillus brevis 5S ribosomal RNA.
VERSION	X02025_1 GI:42965
SOURCE	Lactobacillus brevis
ORGANISM	Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
RESULT 3	LRRNNS LRRNNS 117 bp DNA linear BCT 06-JUN-2003
LOCUS	Lactobacillus brevis 5S ribosomal RNA.
DEFINITION	Lactobacillus brevis 5S ribosomal RNA.
VERSION	X02026_1 GI:42965
SOURCE	Lactobacillus brevis
ORGANISM	Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.